


```

SQ      Sequence 8 AA;

Query Match          94.7%; Score 36; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
      | | | | |
Db      1 FASKYNFD 8

RESULT 2
ABG65702
ID      ABG65702 standard; peptide; 8 AA.
XX
AC      ABG65702;
XX
DT      27-AUG-2002 (first entry)
XX
DE      Plant ICK protein conserved motif 1 #10.
XX
KW      Plant; inhibitor of cyclin dependent kinase; ICK.
XX
OS      Oryza sativa.
XX
PN      WO200228893-A2.
XX
PD      11-APR-2002.
XX
PF      29-JUN-2001; 2001WO-IB001492.
XX
PR      14-JUL-2000; 2000US-0218471P.
XX
PR      13-OCT-2000; 2000US-0241219P.
XX
PA      (CROP-) CROPDESIGN NV.
XX
PI      Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
PI      Hatzfeld Y;
XX
XX      WPI; 2002-471311/50.
XX
PT      Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
PT      to screen substrates, drugs or compounds which modulate ICK activity and
PT      treat disorders characterized by an insufficient or excessive production
PT      of ICK inhibitors.
XX
PS      Disclosure; Page 14; 141pp; English.
XX
CC      This invention relates to the DNA and protein sequences of novel isolated
CC      ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
CC      the invention may be used for treating disorders characterised by
CC      insufficient or excessive production of an ICK inhibitor. The protein of
CC      the invention may also be used to screen for naturally-occurring ICK
CC      substrates, drugs or compounds which modulate ICK activity, as well as to
CC      treat disorders characterised by insufficient or excessive production of
CC      ICK protein, forms which have decreased or aberrant activity compared to
CC      ICK wild type protein. The present sequence represents an inhibitor of
CC      cyclin dependent kinase (ICK) protein of the invention
XX
SQ      Sequence 8 AA;

Query Match          94.7%; Score 36; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
      | | | | |
Db      1 FASKYNFD 8

RESULT 4
AAP01950
ID      AAP01950 standard; protein; 37 AA.
XX
AC      AAP01950;
XX
DT      01-NOV-2001 (first entry)
XX
DE      Rice Cyclin dependent kinase inhibitor (CDKI) clone rds2c.pk0088.c24.
XX
KW      Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
KW      plant growth inhibitor.
XX
OS      Oryza sativa.
XX
XX      Key
XX      Location/Qualifiers
XX      Misc-difference 33
XX      FT

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FT XX /note= "Encoded by GTCA"
FN XX
PD XX WO2000060087-A2.
PD XX 12-OCT-2000.
PF XX
PF XX 06-APR-2000; 2000WO-US009106.
XX XX
XX XX 07-APR-1999; 99US-0128192P.
XX XX
XX XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX XX
XX XX Klein TM, Weng Z, Cahoon RE;
XX XX WPI; 2000-679375/66.
XX XX N-PSDB; AAN02400.
XX XX
XX XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX XX herbicides and plant growth inhibitors.
XX XX
XX XX Claim 10; Fig 1; 58pp; English.
XX XX
XX XX The invention describes a novel isolated polynucleotide comprising a
XX XX nucleotide sequence encoding one of 17 specific cyclin dependent kinase
XX XX inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
XX XX of cell division, growth and death. The nucleotide sequences can be used
XX XX in a vector to transform a host cell to produce the CDKI polypeptide.
XX XX They can also be used in methods for selecting and obtaining a nucleic
XX XX acid sequence that encodes CDKI or affects the level of CDKI expression.
XX XX The encoded protein can be used in a method for evaluating a compound for
XX XX its ability to inhibit the activity of a CDKI. The inhibitors can be used
XX XX as herbicides. They can also be used to inhibit plant growth. The
XX XX polynucleotide sequences can be used in gene mapping and as genetic
XX XX markers. The sequence is the rice CDKI clone rds2c.pk008.024 as described
XX XX in the method of the invention
XX XX
XX XX Sequence 37 AA;
XX XX
XX XX Query Match 94.7%; Score 36; DB 3; Length 37;
XX XX Best Local Similarity 75.0%; Pred. No. 2.1;
XX XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX XX
XX XX QY 1 FXXXYNFD 8
XX XX | | | | |
XX XX 8 FAAKYNFD 15
XX XX
XX XX Db
XX XX
XX XX RESULT 6
XX XX ABE98860
XX XX ID ABB98860 standard; protein; 42 AA.
XX XX
XX XX AC ABB98860;
XX XX
XX XX DT 21-FEB-2003 (first entry)
XX XX
XX XX DE Maize CKI_B C-terminal protein fragment.
XX XX
XX XX KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield;
XX XX KW root size; plant growth; tassel size; ear size; male sterility;
XX XX KW endoreduplication.
XX XX
XX XX OS Zea mays.
XX XX
XX XX PN WO200281623-A2.
XX XX
XX XX PD *17-OCT-2002.
XX XX
XX XX PF 06-NOV-2001; 2001WO-US044038.
XX XX
XX XX PR 07-NOV-2000; 2000US-0246349P.
XX XX
XX XX (PION-) PIONEER HI-BRED INT INC.
XX XX (ARIZ-) ARIZONA BOARD OF REGENTS.
XX XX
XX XX Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;
XX XX WPI; 2003-058511/05.
XX XX
XX XX Novel cyclin-dependent kinase polynucleotides and their encoded proteins,
XX XX involved in cell cycle regulation, and useful for altering cell cycle
XX XX protein content, cell cycle progression, cell number and composition of
XX XX plants.
XX XX
XX XX Example 11; Page 46; 69pp; English.
XX XX
XX XX The present invention relates to maize cyclin-dependent kinase inhibitor

```

CC (CKI), CKI_B, CKI_C and CKI_D. The coding sequences (I) for these
 CC proteins are useful for modulating the activity of CDK in a plant such as
 CC a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton,
 CC rice, barley, oil-seed Brassica and millet. Modulating the activity of
 CC CDK, preferably modulating downward is useful for providing differential
 CC growth in a plant, especially a positive growth advantage and modulating
 CC CDK activity upward is useful for increasing crop yield, root size, plant
 CC growth, tassel size and/or ear size. Modulating CDK activity is also
 CC useful for conferring male sterility and for improving transformation
 CC frequencies by increasing the number of cells in cell division. CDK
 CC activity can also be modulated for modulating endoreduplication in the
 CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the
 CC promoter used is an endosperm-preferred promoter. The cell numbers are
 CC modulated in one or more tissues of a plant, comprising root, seed,
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying
 CC maize CKI interacting proteins, by adding the nucleic acid sequence to
 CC a second nucleic acid sequence encoding a DNA-binding domain. The present
 CC sequence is a C-terminal protein fragment of CKI_B. This sequence
 CC contains a CDK binding region and/or cyclin binding domains
 CC
 XX
 SQ Sequence 42 AA;

Query Match 94.7%; Score 36; DB 6; Length 42;
 Best Local Similarity 75.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXKYNFD 8
 DB 14 FASKYNFD 21

RESULT 7
 ABB98862
 ID ABB98862 standard; protein; 46 AA.
 AC ABB98862;
 XX
 DT 21-FEB-2003 (first entry)
 XX
 DE Maize CKI_D C-terminal protein fragment.
 XX
 KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield;
 KW root size; plant growth; tassel size; ear size; male sterility;
 KW endoreduplication.
 XX
 OS Zea mays.
 XX
 PN WO200281623-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 06-NOV-2001; 2001WO-US044038.
 XX
 PR 07-NOV-2000; 2000US-0246349P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (ARIZ-) ARIZONA BOARD OF REGENTS.
 XX
 PI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;
 XX WPI; 2003-058511/05.
 XX
 PT Novel cyclin-dependent kinase polynucleotides and their encoded proteins,
 PT involved in cell cycle regulation, and useful for altering cell cycle
 PT protein content, cell cycle progression, cell number and composition of
 PT plants.
 XX
 PS Example 11; Page 46; 69pp; English.
 PS
 XX The present invention relates to maize cyclin-dependent kinase inhibitor
 CC (CKI), CKI_B, CKI_C and CKI_D. The coding sequences (I) for these

CC proteins are useful for modulating the activity of CDK in a plant such as
 CC a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton,
 CC rice, barley, oil-seed Brassica and millet. Modulating the activity of
 CC CDK, preferably modulating downward is useful for providing differential
 CC growth in a plant, especially a positive growth advantage and modulating
 CC CDK activity upward is useful for increasing crop yield, root size, plant
 CC growth, tassel size and/or ear size. Modulating CDK activity is also
 CC useful for conferring male sterility and for improving transformation
 CC frequencies by increasing the number of cells in cell division. CDK
 CC activity can also be modulated for modulating endoreduplication in the
 CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the
 CC promoter used is an endosperm-preferred promoter. The cell numbers are
 CC modulated in one or more tissues of a plant, comprising root, seed,
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying
 CC maize CKI interacting proteins, by adding the nucleic acid sequence to
 CC a second nucleic acid sequence encoding a DNA-binding domain. The present
 CC sequence is a C-terminal protein fragment of CKI_D. This sequence
 CC contains a CDK binding region and/or cyclin binding domains
 CC
 XX
 SQ Sequence 46 AA;

Query Match 94.7%; Score 36; DB 6; Length 46;
 Best Local Similarity 75.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXKYNFD 8
 DB 19 FASKYNFD 26

RESULT 8
 AAB26245
 ID AAB26245 standard; protein; 53 AA.
 AC AAB26245;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Corn cyclin-dependent kinase inhibitor #1.
 XX
 KW Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;
 KW cell growth; herbicide.
 XX
 OS Zea mays.
 XX
 PN WO200060087-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US009106.
 XX
 PR 07-APR-1999; 99US-0128192P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Klein TM, Weng Z, Cahoon RE;
 XX WPI; 2000-679375/66.
 DR N-PSDB; AAA95276.
 XX
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 PS
 XX Claim 10; Page 40; 58pp; English.
 XX
 CC The present sequence is the corn cyclin-dependent kinase inhibitor
 CC (CDKI), its coding sequence was isolated by searching a corn silk cDNA
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*
 CC rubrum, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of

CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX
 SQ Sequence 53 AA;

Query Match 94.7%; Score 36; DB 3; Length 53;
 Best Local Similarity 75.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 | | | | |
 Db 30 FASKYNFD 37

RESULT 9
 AAP01940
 ID AAP01940 standard; protein; 53 AA.
 AC AAP01940;
 XX
 XX 01-NOV-2001 (first entry)
 DT
 DE Corn Cyclin dependent kinase inhibitor (CDKI) clone csln.pk0050.e6.
 XX
 XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; corn;
 KW plant growth inhibitor.
 KW
 XX
 XX Zea mays.
 OS
 XX WO200060087-A2.
 PN
 XX 12-OCT-2000.
 PD
 XX 06-APR-2000; 2000WO-US009106.
 PF
 XX 07-APR-1999; 99US-0128192P.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Klein TM, Weng Z, Cahoon RE;
 PI
 XX WPI; 2000-679375/66.
 DR
 DR N-PSDB; AAN02390.
 XX
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 PT
 XX Claim 10; Page 40; 58pp; English.

The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the corn CDKI clone csln.pk0050.e6 as described
 CC in the method of the invention
 XX

SQ Sequence 53 AA;
 Query Match 94.7%; Score 36; DB 3; Length 53;
 Best Local Similarity 75.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 | | | | |
 Db 30 FASKYNFD 37

RESULT 10
 ABG65674
 ID ABG65674 standard; protein; 116 AA.
 XX

AC ABG65674;
 XX
 XX 07-AUG-2003 (revised)
 DT 27-AUG-2002 (first entry)
 XX
 XX Corn ICK 1 protein.
 DE
 XX
 XX Plant; inhibitor of cyclin dependent kinase; ICK.
 KW
 XX
 XX Zea mays.

PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 XX 29-JUN-2001; 2001WO-IB001492.
 PF
 XX 14-JUL-2000; 2000US-0218471P.
 PR
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 XX (CROP-) CROPDESIGN NV.
 PA

XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 PI
 XX WPI; 2002-471311/50.
 DR
 DR N-PSDB; ABK93954.
 XX

PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX

PS Claim 48; Fig 4; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention. (Updated on 07-
 CC AUG-2003 to correct OS field.)
 XX

SQ Sequence 116 AA;

Query Match 94.7%; Score 36; DB 5; Length 116;
 Best Local Similarity 75.0%; Pred. No. 7;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 | | | | |
 Db 89 FASKYNFD 96

RESULT 11
 AAB26250
 ID AAB26250 standard; protein; 125 AA.
 XX
 XX AAB26250;
 XX

XX 17-JAN-2001 (first entry)
 DT
 XX Corn cyclin-dependent kinase inhibitor #3.
 DE

XX Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;
 KW cell growth; herbicide.
 XX
 OS Zea mays.
 XX
 PN WO200060087-A2.
 XX
 PD 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US009106.
 XX
 XX 07-APR-1999; 99US-0128192P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Klein TM, Weng Z, Cahoon RE;
 XX
 XX WPI; 2000-679375/66.
 DR N-PSDB; AAA95281.
 XX
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 PS Claim 10; Fig 1; 58pp; English.
 XX
 CC The present sequence is the corn cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a contig comprising
 CC cDNA from corn roots and ear leaf sheath for sequences similar to those
 CC encoding the CDKI from *Chenopodium rubrum*, *Caenorhabditis elegans* and
 CC *Arabidopsis thaliana*. CDKI is involved in the cell cycle, and may promote
 CC or inhibit cell division and growth. The protein and its coding sequence
 CC are useful in the production of transgenic plants which produce increased
 CC or decreased amounts of the CDKI protein, in the identification of
 CC herbicides, in genetic and physical mapping and in the isolation of the
 CC CDKI gene in other organisms
 XX
 XX Sequence 125 AA;
 Query Match 94.7%; Score 36; DB 3; Length 125;
 Best Local Similarity 75.0%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 97 FASKYNFD 104
 RESULT 12
 ID AAB26249 standard; protein; 126 AA.
 XX
 AC AAB26249;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Corn cyclin-dependent kinase inhibitor #2.
 XX
 KW Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;
 KW cell growth; herbicide.
 XX
 OS Zea mays.
 XX
 PN WO200060087-A2.
 XX
 PD 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US009106.
 XX
 XX 07-APR-1999; 99US-0128192P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;
 XX
 DR WPI; 2000-679375/66.
 DR N-PSDB; AAA95280.
 XX
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 PS Claim 10; Fig 1; 58pp; English.
 XX
 CC The present sequence is the corn cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a corn silk cDNA
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX
 XX Sequence 126 AA;
 Query Match 94.7%; Score 36; DB 3; Length 126;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 99 FASKYNFD 106
 RESULT 13
 ID ABG65692 standard; protein; 226 AA.
 XX
 AC ABG65692;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Rice OsGICK5 protein.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS *Oryza sativa*.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93981.
 XX
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Claim 48; Page 139-140; 141pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of

CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention

XX Sequence 226 AA;

Query Match 94.7%; Score 36; DB 5; Length 226;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 | | | | |
 Db 196 FAKYNFD 203

RESULT 14

ABB98757
 ID ABB98757 standard; protein; 256 AA.

XX AC ABB98757;

XX DT 21-FEB-2003 (first entry)

XX DE Maize CKI_B.

XX KW Maize; cyclin-dependent kinase inhibitor; CKI; CKI_B; plant; corn;
 KW crop yield; root size; plant growth; tassel size; ear size;
 KW male sterility; endoreduplication.

XX OS Zea mays.

XX FH Key Location/Qualifiers
 FT Domain 1..7
 FT /note= "Conserved domain"

XX FN WO200281623-A2.

XX PD 17-OCT-2002.

XX XX 06-NOV-2001; 2001WO-US044038.

XX PR 07-NOV-2000; 2000US-0246349P.

XX PA (PION-) PIONEER HI-BRED INT INC.
 XX (ARIZ-) ARIZONA BOARD OF REGENTS.

XX PI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;

XX DR WPI; 2003-058511/05.
 XX N-PSDB; ABV74603.

XX PT Novel cyclin-dependent kinase polynucleotides and their encoded proteins,
 PT involved in cell cycle regulation, and useful for altering cell cycle
 PT protein content, cell cycle progression, cell number and composition of
 PT plants.

XX PS Claim 12; Page 65-66; 69pp; English.

XX CC The present sequence is maize cyclin-dependent kinase inhibitor (CKI),
 CC CKI_B. The coding sequence for this protein (I) is useful for modulating
 CC the activity of cyclin-dependent kinase (CDK) in a plant such as a corn,
 CC soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice,
 CC barley, oil-seed Brassica and millet. Modulating the activity of CDK,
 CC preferably modulating downward is useful for providing differential
 CC growth in a plant, especially a positive growth advantage and modulating
 CC CDK activity upward is useful for increasing crop yield, root size, plant
 CC growth, tassel size and/or ear size. Modulating CDK activity is also
 CC useful for conferring male sterility and for improving transformation
 CC frequencies by increasing the number of cells in cell division. CDK
 CC activity can also be modulated for modulating endoreduplication in the

CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the
 CC promoter used is an endosperm-preferred promoter. The cell numbers are
 CC modulated in one or more tissues of a plant, comprising root, seed,
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves,
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,
 CC pericarp, meristematic or leaf cells. (I) is also useful for identifying
 CC maize CKI interacting proteins, by adducting the nucleic acid sequence to
 CC a second nucleic acid sequence encoding a DNA-binding domain

XX SQ Sequence 256 AA;

Query Match 94.7%; Score 36; DB 6; Length 256;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 | | | | |

Db 228 FASKYNFD 235

RESULT 15

ABG65670

ID ABG65670 standard; protein; 262 AA.

XX AC ABG65670;

XX DT 27-AUG-2002 (first entry)

XX DE OsICK 2 protein.

XX KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Oryza sativa.

XX PN WO200228893-A2.

XX PD 11-APR-2002.

XX PF 29-JUN-2001; 2001WO-IB001492.

XX PR 14-JUL-2000; 2000US-0218471P.

XX PR 13-OCT-2000; 2000US-0241219P.

XX XX (CROP-) CROPDDESIGN NV.

XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX PI Hatzfeld Y;

XX DR WPI; 2002-471311/50.

XX DR N-PSDB; ABX93958.

XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.

XX PS Claim 48; Fig 3; 141pp; English.

XX CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention

XX SQ Sequence 262 AA;

Query Match 94.7%; Score 36; DB 5; Length 262;
 Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8
| | | | |
Db 233 FAKYNFD 240

Search completed: October 26, 2004, 15:36:51
Job time : 45.6154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds
(without alignments)
40.099 Million cell updates/sec

Title: US-09-574-735C-34
Perfect score: 38
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62
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Searched: 478139 seqs, 66318000 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	34	89.5	223	4	US-09-526-597D-6
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4	31	81.6	385	4	US-09-248-796A-16581
5	31	81.6	648	4	US-09-538-032-536
6	31	81.6	814	1	US-08-233-788A-42
7	30	78.9	85	4	US-09-270-767-61052
8	30	78.9	147	4	US-09-270-767-32252
9	30	78.9	147	4	US-09-270-767-47469
10	30	78.9	170	4	US-09-270-767-34019
11	30	78.9	170	4	US-09-270-767-49236
12	30	78.9	209	4	US-09-526-597D-2
13	30	78.9	348	4	US-09-328-352-7509
14	30	78.9	363	4	US-09-270-767-45543
15	30	78.9	410	3	US-09-140-466-2
16	30	78.9	682	4	US-09-252-991A-30482
17	30	78.9	1835	3	US-09-404-650-5
18	30	78.9	1835	4	US-09-495-714C-2
19	30	78.9	1912	4	US-07-745-206A-7
20	30	78.9	1968	1	US-08-455-543A-45
21	30	78.9	1968	1	US-08-223-305C-45
22	30	78.9	1968	2	US-08-311-363-7
23	30	78.9	1977	4	US-09-495-714C-4
24	30	78.9	1985	4	US-09-495-714C-6
25	30	78.9	2161	1	US-07-745-206A-2
26	30	78.9	2161	1	US-08-455-543A-49
27	30	78.9	2161	1	US-08-455-543A-51

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Sequence 49, Appl
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Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 50, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 22886, A
Sequence 14, Appl
Sequence 15, Appl
Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-526-597D-4
; Sequence 4, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-526-597D-4

Query Match 89.5%; Score 34; DB 4; Length 222;
Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8
Db 197 FMEKYNFD 204

RESULT 2
US-09-526-597D-6
; Sequence 6, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-526-597D-6

Query Match 89.5%; Score 34; DB 4; Length 223;

Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 198 FMEKYNFD 205

RESULT 3

US-09-248-796A-18335
; Sequence 18335, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18335
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18335

Query Match 81.6%; Score 31; DB 4; Length 118;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 34 FLSKFNFD 41

RESULT 4

US-09-248-796A-16581
; Sequence 16581, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16581
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16581

Query Match 81.6%; Score 31; DB 4; Length 385;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 106 FNDKYNFD 113

RESULT 5

US-09-538-092-536
; Sequence 536, Application US/09538092

Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 536
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YLR098C
US-09-538-092-536

Query Match 81.6%; Score 31; DB 4; Length 648;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 620 FALYFNFD 627

RESULT 6

US-08-233-788A-42
; Sequence 42, Application US/08233788A
; Patent No. 5635617
; GENERAL INFORMATION:
; APPLICANT: Doran, James L.
; APPLICANT: Kay, William W.
; APPLICANT: Collinson, Karen S.
; APPLICANT: Clouthier, Sharon C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,788A
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 920043.403C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 814 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-42

Query Match      81.6%; Score 31; DB 1; Length 814;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 21 FSRQYNFD 28

RESULT 7
US-09-270-767-61052
; Sequence 61052, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61052
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61052

Query Match      78.9%; Score 30; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 30 KYNFD 34

RESULT 8
US-09-270-767-32252
; Sequence 32252, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32252
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32252

Query Match      78.9%; Score 30; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 132 KYNFD 136

RESULT 9
US-09-270-767-47469
; Sequence 47469, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47469
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47469

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Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 132 KYNFD 136

RESULT 10
US-09-270-767-34019
; Sequence 34019, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34019
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34019

Query Match      78.9%; Score 30; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
Db 103 KYNFD 107

RESULT 11
US-09-270-767-49236
; Sequence 49236, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49236
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49236

Query Match      78.9%; Score 30; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 KYNFD 8
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Db 103 KYNFD 107

RESULT 12
US-09-526-597D-2
; Sequence 2, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-2

Query Match 78.9%; Score 30; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
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Db 186 KYNFD 190

RESULT 13
US-09-328-352-7509
; Sequence 7509, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7509
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7509

Query Match 78.9%; Score 30; DB 4; Length 348;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
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Db 95 KYNFD 99

RESULT 14
US-09-270-767-45543
; Sequence 45543, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45543
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45543

Query Match 78.9%; Score 30; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
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Db 283 KYNFD 287

RESULT 15
US-09-140-466-2
; Sequence 2, Application US/09140466
; Patent No. 6288160
; GENERAL INFORMATION:
; APPLICANT: CLOUGH, BARBARA
; APPLICANT: PREISER, PETER
; APPLICANT: WILSON, ROBERT
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
; FILE REFERENCE: N68837B GCW FJC DP
; CURRENT APPLICATION NUMBER: US/09/140,466
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/056,246
; EARLIER FILING DATE: 1997-08-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-140-466-2

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KYNFD 8
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Db 160 KYNFD 164

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 115.077 Seconds
(without alignments)
22.507 Million cell updates/sec

Title: US-09-574-735C-34

Perfect score: 38

Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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2	36	94.7	221	15	US-10-425-114-69245	Sequence 69245, A
3	36	94.7	226	15	US-10-333-006-55	Sequence 55, Appl
4	36	94.7	256	11	US-09-993-308-2	Sequence 2, Appl
5	36	94.7	256	11	US-09-993-808B-2	Sequence 2, Appl
6	36	94.7	262	15	US-10-333-006-10	Sequence 10, Appl
7	36	94.7	263	15	US-10-425-114-63204	Sequence 63204, A
8	36	94.7	354	16	US-10-437-963-122432	Sequence 122432, A
9	36	94.7	417	16	US-10-437-963-195115	Sequence 195115, A
10	36	94.7	423	16	US-10-437-963-122443	Sequence 122443, A
11	35	92.1	176	15	US-10-424-599-212181	Sequence 212181, A
12	35	92.1	196	9	US-09-733-507-16	Sequence 16, Appl
13	35	92.1	196	15	US-10-451-139-15	Sequence 15, Appl

14	35	92.1	440	13	US-10-011-588-31	Sequence 31, Appl
15	35	92.1	441	13	US-10-011-588-11	Sequence 11, Appl
16	35	92.1	824	13	US-10-011-588-33	Sequence 33, Appl
17	35	92.1	1275	15	US-10-452-024-167	Sequence 167, Appl
18	35	92.1	1276	14	US-10-273-898-66	Sequence 66, Appl
19	35	92.1	1276	14	US-10-354-774-66	Sequence 66, Appl
20	35	92.1	1276	14	US-10-271-012-66	Sequence 66, Appl
21	35	92.1	1276	15	US-10-452-024-4	Sequence 4, Appl
22	35	92.1	1276	15	US-10-452-024-164	Sequence 164, Appl
23	35	92.1	1276	15	US-10-452-024-168	Sequence 168, Appl
24	35	92.1	1276	15	US-10-205-516-8	Sequence 8, Appl
25	35	92.1	1276	16	US-10-729-132-66	Sequence 66, Appl
26	35	92.1	1276	16	US-10-729-039-66	Sequence 66, Appl
27	35	92.1	1285	15	US-10-452-024-165	Sequence 165, Appl
28	35	92.1	1285	15	US-10-452-024-166	Sequence 166, Appl
29	35	92.1	1286	15	US-10-205-516-22	Sequence 22, Appl
30	35	92.1	1664	14	US-10-369-493-22428	Sequence 22428, A
31	34	89.5	90	15	US-10-333-006-13	Sequence 13, Appl
32	34	89.5	93	15	US-10-333-006-15	Sequence 15, Appl
33	34	89.5	137	9	US-09-733-507-14	Sequence 14, Appl
34	34	89.5	137	15	US-10-451-139-13	Sequence 13, Appl
35	34	89.5	190	9	US-09-993-308-4	Sequence 4, Appl
36	34	89.5	190	11	US-09-993-808B-4	Sequence 4, Appl
37	34	89.5	191	9	US-09-733-507-2	Sequence 2, Appl
38	34	89.5	191	9	US-09-733-507-10	Sequence 10, Appl
39	34	89.5	191	15	US-10-451-139-2	Sequence 2, Appl
40	34	89.5	194	15	US-10-333-006-44	Sequence 44, Appl
41	34	89.5	194	16	US-10-437-963-120870	Sequence 120870, A
42	34	89.5	196	15	US-10-451-139-22	Sequence 22, Appl
43	34	89.5	205	15	US-10-424-599-235800	Sequence 235800, A
44	34	89.5	212	9	US-09-733-507-12	Sequence 12, Appl
45	34	89.5	212	15	US-10-451-139-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-333-006-14
; Sequence 14, Application US/103333006
; Publication No: US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)-(11)
; OTHER INFORMATION: Xaa = any amino acid
US-10-333-006-14

Query Match 94.7%; Score 36; DB 15; Length 116;
Best Local Similarity 75.0%; Pred.No. 12;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 89 FASKYNFD 96

RESULT 2
US-10-425-114-69245
; Sequence 69245, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69245
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3079-036-F9_FLI.pep
US-10-425-114-69245

Query Match 94.7%; Score 36; DB 15; Length 221;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 193 FASKYNFD 200

RESULT 3
US-10-333-006-55
; Sequence 55, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: probe or primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119)..(119)
; OTHER INFORMATION: Xaa = any amino acid

US-10-333-006-55

Query Match 94.7%; Score 36; DB 15; Length 226;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 196 FASKYNFD 203

RESULT 4
US-09-993-308-2
; Sequence 2, Application US/09993308
; Patent No. US20020159435A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Larkins, Brian A.
; APPLICANT: Dilkes, Brian R.
; APPLICANT: Sun, Yuejin
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides and Uses Thereof
; FILE REFERENCE: 1146
; CURRENT APPLICATION NUMBER: US/09/993,308
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,349
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays
US-09-993-308-2

Query Match 94.7%; Score 36; DB 9; Length 256;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
Db 228 FASKYNFD 235

RESULT 5
US-09-993-808B-2
; Sequence 2, Application US/09993808B
; Publication No. US20040003433A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; APPLICANT: Lowe, Keith
; APPLICANT: Sun, Yuejin
; APPLICANT: Dilkes, Brian
; APPLICANT: Larkins, Brian
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1146
; CURRENT APPLICATION NUMBER: US/09/993,808B
; CURRENT FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(256)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-993-808B-2

Query Match 94.7%; Score 36; DB 11; Length 256;
Best Local Similarity 75.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
| | | | |
Db 228 FASKYNFD 235

RESULT 6

US-10-333-006-10
; Sequence 10, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1111 S.
; APPLICANT: Petes Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IS01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-10

Query Match 94.7%; Score 36; DB 15; Length 262;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
| | | | |
Db 233 FASKYNFD 240

RESULT 7

US-10-425-114-63204
; Sequence 63204, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63204
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17355F05_FLI1.pcp
US-10-425-114-63204

Query Match 94.7%; Score 36; DB 15; Length 263;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
| | | | |
Db 235 FASKYNFD 242

RESULT 8

US-10-437-963-122432
; Sequence 122432, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122432
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2535C.1.pcp
US-10-437-963-122432

Query Match 94.7%; Score 36; DB 16; Length 354;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
| | | | |
Db 219 FASKYNFD 226

RESULT 9

US-10-437-963-195115
; Sequence 195115, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195115
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91095C.1.pcp
US-10-437-963-195115

Query Match 94.7%; Score 36; DB 16; Length 417;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 388 FAKYNFD 395

RESULT 10
 US-10-437-963-122443
 ; Sequence 122443, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 122443
 ; LENGTH: 423
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2536C.1.pep
 US-10-437-963-122443

Query Match 94.7%; Score 36; DB 16; Length 423;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 232 FAKYNFD 239

RESULT 11
 US-10-424-599-212181
 ; Sequence 212181, Application US/10424599
 ; Publication No. US20040301072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 212181
 ; LENGTH: 176
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_33625C.1.pep
 US-10-424-599-212181

Query Match 92.1%; Score 35; DB 15; Length 176;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 152 FTEKYNFD 159

RESULT 12
 US-09-733-507-16
 ; Sequence 16, Application US/09733507
 ; Patent No. US20010025379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
 ; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
 ; FILE REFERENCE: 81601-3
 ; CURRENT APPLICATION NUMBER: US/09/733,507
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: CA 2,256,121
 ; PRIOR FILING DATE: 1998-12-31
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 196
 ; TYPE: PRT
 ; ORGANISM: Chenopodium rubrum
 US-09-733-507-16

Query Match 92.1%; Score 35; DB 9; Length 196;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 171 FSEKYNFD 178

RESULT 13
 US-10-451-139-15
 ; Sequence 15, Application US/10451139
 ; Publication No. US20040098763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WANG, HONG
 ; APPLICANT: ZHOU, YONGMING
 ; APPLICANT: FOMKE, LAREY C.
 ; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
 ; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
 ; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
 ; FILE REFERENCE: 4810-62237
 ; CURRENT APPLICATION NUMBER: US/10/451,139
 ; CURRENT FILING DATE: 2003-06-18
 ; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US 60/255,908
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 196
 ; TYPE: PRT
 ; ORGANISM: Chenopodium rubrum
 US-10-451-139-15

Query Match 92.1%; Score 35; DB 15; Length 196;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 171 FSEKYNFD 178

RESULT 14
 US-10-011-588-31
 ; Sequence 31, Application US/10011588
 ; Publication No. US20020168727A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Leonard
 ; APPLICANT: Jensen, Melody

;; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
;; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
;; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
;; FILE REFERENCE: A34796 067252.0113
;; CURRENT APPLICATION NUMBER: US/10/011,588
;; CURRENT FILING DATE: 2002-03-29
;; PRIOR APPLICATION NUMBER: 09/910,186
;; PRIOR FILING DATE: 2001-07-20
;; PRIOR APPLICATION NUMBER: 09/611,419
;; PRIOR FILING DATE: 2000-07-06
;; PRIOR APPLICATION NUMBER: 60/246,744
;; PRIOR FILING DATE: 2000-11-06
;; PRIOR APPLICATION NUMBER: 60/311,966
;; PRIOR FILING DATE: 2001-08-09
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 31
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Recombinant protein encoded by SEQ ID NO:30
US-10-011-588-31

Query Match 92.1%; Score 35; DB 13; Length 440;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXXKYNFD 8
| | | | |
Db 324 FSEKYNFD 331

RESULT 15

US-10-011-588-11
;; Sequence 11, Application US/10011588
;; Publication No. US20020168727A1
;; GENERAL INFORMATION:
;; APPLICANT: Jensen, Melody
;; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
;; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
;; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
;; FILE REFERENCE: A34796 067252.0113
;; CURRENT APPLICATION NUMBER: US/10/011,588
;; CURRENT FILING DATE: 2002-03-29
;; PRIOR APPLICATION NUMBER: 09/910,186
;; PRIOR FILING DATE: 2001-07-20
;; PRIOR APPLICATION NUMBER: 09/611,419
;; PRIOR FILING DATE: 2000-07-06
;; PRIOR APPLICATION NUMBER: 60/246,744
;; PRIOR FILING DATE: 2000-11-06
;; PRIOR APPLICATION NUMBER: 60/311,966
;; PRIOR FILING DATE: 2001-08-09
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 441
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic botulinum neurotoxin light chain of
;; OTHER INFORMATION: serotype D based on wild-type clostridium
;; OTHER INFORMATION: botulinum sequence
US-10-011-588-11

Query Match 92.1%; Score 35; DB 13; Length 441;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXXKYNFD 8
| | | | |
Db 325 FSEKYNFD 332

Search completed: October 26, 2004, 15:33:29
Job time : 116.077 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds
(without alignments)
69.490 Million cell updates/sec

Title: US-09-574-735C-34
Perfect score: 38
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	196	2 T09968	cyclin-dependent k
2	35	92.1	627	2 D96956	ntcR family transc
3	35	92.1	1276	2 S11455	botulinum neurotox
4	35	92.1	1285	2 S70582	botulinum neurotox
5	35	92.1	1664	2 S67250	DNA-directed RNA p
6	34	89.5	191	2 T01132	cyclin-dependent k
7	34	89.5	699	2 A38368	chitinase (EC 3.2.
8	34	89.5	1635	2 T14075	chitinase (EC 3.2.
9	32	84.2	195	2 H96532	hypothetical prote
10	31	81.6	272	2 S71252	lectin-like protei
11	31	81.6	374	2 T10349	very-late factor 1
12	31	81.6	480	2 T08866	hypothetical prote
13	31	81.6	603	2 G84554	probable acyl-CoA
14	31	81.6	648	2 S97733	transcription acti
15	31	81.6	814	1 C40618	fimbrial outer mem
16	31	81.6	838	2 AC1054	outer membrane fil
17	31	81.6	1050	2 H90316	hypothetical prote
18	30	78.9	114	2 AC3246	hypothetical prote
19	30	78.9	149	2 A70325	hypothetical prote
20	30	78.9	209	2 T46140	hypothetical prote
21	30	78.9	232	2 F84576	hypothetical prote
22	30	78.9	251	2 T40710	hypothetical prote
23	30	78.9	260	2 D64419	hypothetical prote
24	30	78.9	265	2 T29973	hypothetical prote
25	30	78.9	286	2 B90546	hypothetical prote
26	30	78.9	302	2 B84979	sulfate adenylyltr
27	30	78.9	315	2 H84938	flagellar motor sw
28	30	78.9	321	2 AB1316	heptaprenyl diphos
29	30	78.9	321	2 AB1688	heptaprenyl diphos

30 78.9 330 2 C71180 probable N-acetyl-D-2-hydroxy-acid d
31 30 78.9 331 2 F64047 probable exported
32 30 78.9 334 2 A10284 hypothetical prote
33 30 78.9 345 2 T33906 hypothetical prote
34 30 78.9 365 2 E30039 secretory protein
35 30 78.9 399 2 S27879 hypothetical prote
36 30 78.9 408 2 T18813 hypothetical prote
37 30 78.9 410 1 I40755 trigger factor 2 (translation elonga
38 30 78.9 410 2 S72277 trigger factor 2 (translation elonga
39 30 78.9 413 2 A21633 trigger factor 2 (translation elonga
40 30 78.9 444 2 H81437 xylulokinase homol
41 30 78.9 487 2 E39895 phenylalanine-tRNA
42 30 78.9 552 2 T28752 probable solute-bi
43 30 78.9 609 2 H83419 hypothetical prote
44 30 78.9 617 2 H84957 NADH2 dehydrogenas
45 30 78.9 644 2 S44478

ALIGNMENTS

RESULT 1

T09968
cyclin-dependent kinase inhibitor protein - red goosefoot

C:Species: Chenopodium rubrum (red goosefoot)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09968

R:Fountain, M.D.; Renz, A.; Beck, E.

A:Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic

A:Reference number: Z16910

A:Accession: T09968

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-136 <FOU>

A:Cross-references: UNIPROT:O48597; EMBL:AJ002173

A:Experimental source: photoautotrophic cells derived from hypocotyl tissue

C:Genetics:

A:Gene: CDK11

C:Keywords: protein kinase inhibitor

Query Match 92.1%; Score 35; DB 2; Length 196;

Best Local Similarity 75.0%; Pred. No. 4;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8

DB 171 FSEKYNFD 178

RESULT 2

D96956
ntcR family transcription regulator (PAS and AAA domains) [imported] - Clostridium acet

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: D96956

R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D96956

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KUR>

A:Cross-references: UNIPROT:Q97LU5; GB:AE001437; PIDN:AAK78439.1; PID:G15023316; GSPDB:

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0459

Query Match 92.1%; Score 35; DB 2; Length 627;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 89.5%; Score 34; DB 2; Length 191;
Best Local Similarity 75.0%; Pred. No. 64; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8
| | | | |
Db 167 FKXKYNFD 174

RESULT 7
A38368
chitinase (EC 3.2.1.14) precursor - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38368
R;Watanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.
J. Biol. Chem. 265, 15659-15665, 1990
A;Title: Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed its evolution
A;Reference number: A38368; MUID:90368776; PMID:2203782
A;Accession: A38368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-699 <WAT>
A;Cross-references: UNIPROT:P20533; GB:M57601; GB:J05599; NID:gl066341; PIDN:AAA81528.1;
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 699;
Best Local Similarity 75.0%; Pred. No. 24; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8
| | | | |
Db 190 FLKYNFD 197

RESULT 8
T14075
chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A;Reference number: Z17872
A;Accession: T14075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1635
A;Cross-references: UNIPROT:O17412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AA8B
C;Genetics:
A;Gene: CHT2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 1635;
Best Local Similarity 75.0%; Pred. No. 58; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 2;

QY 1 FXXKYNFD 8
| | | | |
Db 1365 FIEKYNFD 1372

RESULT 9
H96532
hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96532
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96532
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195 <STO>
A;Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:gl0120423; PIDN:AAG13048.1; GSPDB:
C;Genetics:
A;Gene: F14J22.14
A;Map position: 1

Query Match 84.2%; Score 32; DB 2; Length 195;
Best Local Similarity 62.5%; Pred. No. 17; Mismatches 1; Indels 2; Gaps 0;
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8
| | | | |
Db 170 FTEKYNFD 177

RESULT 10
S71252
lectin-like protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S71252
R;Herve, C.; Lescure, B.
submitted to the EMBL Data Library, September 1995
A;Description: An Arabidopsis thaliana cDNA encoding a lectin like protein.
A;Reference number: S71252
A;Accession: S71252
A;Molecule type: mRNA
A;Residues: 1-272 <HER>
A;Cross-references: UNIPROT:Q39205; EMBL:X91359; NID:g995618; PID:g995619
C;Superfamily: plant lectin
C;Keywords: lectin

Query Match 81.6%; Score 31; DB 2; Length 272;
Best Local Similarity 62.5%; Pred. No. 39; Mismatches 1; Indels 2; Gaps 0;
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8
| | | | |
Db 18 FAVKFNFD 25

RESULT 11
T10349
very-late factor 1 protein - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OPMNV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10349
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10349
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-374 <HR>
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59079.1; PID:gi9111326

Query Match 81.6%; Score 31; DB 2; Length 374;
Best Local Similarity 62.5%; Pred. No. 54; Mismatches 1; Indels 2; Gaps 0;
Matches 5; Conservative 1;

QY 1 FXXKYNFD 8
 Db 335 YLKNYFD 342

RESULT 12

T08866
 hypothetical protein A_TM017A05.12 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08866
 R:Waterston, R.
 submitted to the EMBL Data Library, October 1997
 A:Reference number: Z16500
 A:Accession: T08866
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-480 <WAT>
 A:Cross-references: UNIPROT:Q9SEY5; EMBL:AF024504; NID:G2435510; PID:G2435522; GSPDB:GNQ
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: ATSP:A_TM017A05.12
 A:Map position: 4
 C:Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology
 F:7-470/Domain: acetate-CoA ligase homology <ACL>

Query Match 81.6%; Score 31; DB 2; Length 480;
 Best Local Similarity 62.5%; Pred. No. 70;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 88 FASKYSFD 95

RESULT 13

G84554
 Probable acyl-CoA synthetase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84554
 M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84554
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-603 <STO>
 A:Cross-references: UNIPROT:Q9SEY5; GB:AB002093; NID:G6598797; PIDN:AAF18674.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g17650
 A:Map position: 2
 C:Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology

Query Match 81.6%; Score 31; DB 2; Length 603;
 Best Local Similarity 62.5%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 211 FASKYSFD 218

RESULT 14

S59723
 transcription activator CHA4 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein L2552; protein YLR098C
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
 C:Accession: S59723; S64932; S72236

R;Schjerling, P.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S59723
 A:Accession: S59723
 A:Molecule type: DNA
 A:Residues: 1-648 <SCH>
 A:Cross-references: UNIPROT:P43634; EMBL:Z49975; NID:G986706; PIDN:CAA90276.1; PID:G9867
 R;Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Ansoerge, W.; Voss, H.
 submitted to the Protein Sequence Database, May 1996

A:Reference number: S64920
 A:Accession: S64932
 A:Molecule type: DNA
 A:Residues: 1-648 <BEN>

A:Cross-references: EMBL:Z73270; NID:gl360478; PIDN:CAA97662.1; PID:e245801; PID:gl36047
 R;Holmberg, S.; Schjerling, P.
 Genetics 144, 467-478, 1996

A:Title: Chafp of Saccharomyces cerevisiae activates transcription via serine/threonine
 A:Reference number: S72236; MUID:97044442; PMID:8889513
 A:Accession: S72236
 A:Molecule type: DNA
 A:Residues: 1-648 <HOL>

A:Cross-references: EMBL:Z49975; NID:G986706; PIDN:CAA90276.1; PID:G986707
 C:Genetics:
 A:Gene: SGD:CHA4

A:Cross-references: SGD:S0004088; MIPS:YLR098C
 A:Map position: 12R
 C:Function:

A:Description: activation of CHA1; binds to UAS1(CHA) and UAS2(CHA) elements in CHA1 pro
 C:Superfamily: GAL4 zinc binuclear cluster homology
 C:Keywords: DNA binding; nucleus
 F:39-75/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 81.6%; Score 31; DB 2; Length 648;
 Best Local Similarity 62.5%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 620 FALEYNFD 627

RESULT 15

C40618
 fimbrial outer membrane protein homolog SefC - Salmonella enteritidis
 C:Species: Salmonella enteritidis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: C40618
 R;Clouthier, S.C.; Muller, K.H.; Doran, J.L.; Collinson, S.K.; Kay, W.W.
 J. Bacteriol. 175, 2523-2533, 1993
 A:Title: Characterization of three fimbrial genes, sefABC, of Salmonella enteritidis.
 A:Reference number: A40618; MUID:93239677; PMID:8097515
 A:Contents: 27655-3b
 A:Accession: C40618
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-814 <CLO>
 A:Cross-references: UNIPROT:P33388; GB:L11010; NID:G310649; PIDN:AAA27221.1; PID:G310650
 A:Note: sequence extracted from NCBI backbone (NCBIN:130387, NCBIP:130397)
 C:Superfamily: outer membrane usher protein fimb
 C:Keywords: membrane protein

Query Match 81.6%; Score 31; DB 1; Length 814;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 Db 21 FSRQYNFD 28

Search completed: October 26, 2004, 15:40:06
 Job time : 14.0769 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 44.6154 Seconds
(without alignments)
103.171 Million cell updates/sec

Title: US-09-574-735C-34
Perfect score: 38
Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	94.7	262	2	Q6Z6G5	Q6Z6G5 oryza sativ
2	36	94.7	262	2	BAD17213	BAD17213 oryza sat
3	35	92.1	113	2	O17419	O17419 anopheles s
4	35	92.1	196	2	O48597	O48597 chenopodium
5	35	92.1	207	2	O8GUA2	O8GUA2 nicotiana t
6	35	92.1	442	2	Q8EV36	Q8EV36 mycoplasma
7	35	92.1	627	2	Q97LU5	Q97LU5 clostridium
8	35	92.1	1275	2	Q9QTG7	Q9QTG7 clostridium
9	35	92.1	1276	1	BXD_CLOBO	P19321 clostridium
10	35	92.1	1285	2	Q45967	Q45967 clostridium
11	35	92.1	1285	2	O9LBR1	O9LBR1 clostridium
12	35	92.1	1640	2	O759A3	O759A3 ashbya goss
13	35	92.1	1640	2	AA552294	AA552294 ashbya go
14	35	92.1	1643	2	Q6FV16	Q6FV16 candida gla
15	35	92.1	1653	2	Q6CIX4	Q6CIX4 kluyveromyc
16	35	92.1	1664	1	RPAL_YEAST	P10964 saccharomyc
17	34	89.5	113	2	O17414	O17414 anopheles g
18	34	89.5	156	2	Q93YF6	Q93YF6 nicotiana t
19	34	89.5	163	2	Q93Y92	Q93Y92 nicotiana t
20	34	89.5	185	2	Q8GT28	Q8GT28 lycopersico
21	34	89.5	189	2	Q9LRY0	Q9LRY0 arabidopsis
22	34	89.5	191	2	O04154	O04154 arabidopsis
23	34	89.5	191	2	O82809	O82809 arabidopsis
24	34	89.5	191	2	O8LDX1	O8LDX1 arabidopsis
25	34	89.5	196	2	O9LJL5	O9LJL5 arabidopsis
26	34	89.5	210	2	Q8GT29	Q8GT29 lycopersico
27	34	89.5	222	2	Q9FKB5	Q9FKB5 arabidopsis
28	34	89.5	242	2	Q7XDH8	Q7XDH8 oryza sativ
29	34	89.5	242	2	Q9FW65	Q9FW65 oryza sativ
30	34	89.5	286	2	Q8GYJ3	Q8GYJ3 arabidopsis
31	34	89.5	286	2	Q94CM0	Q94CM0 arabidopsis

32 34 89.5 289 2 O48846 O48846 arabidopsis
33 34 89.5 474 2 O86LZ2 O86LZ2 lutzomyia l
34 34 89.5 484 2 Q9W092 Q9W092 grosophila
35 34 89.5 553 2 Q704Y2 Q704Y2 lacanobia o
36 34 89.5 553 2 CAF05663 CAF05663 lacanobia o
37 34 89.5 557 2 Q8MTK0 Q8MTK0 chorisoneu
38 34 89.5 699 1 CH11_BACCI P20533 bacillus ci
39 34 89.5 699 2 O48494 O48494 kurthia zop
40 34 89.5 717 2 O9KHB3 O9KHB3 bacillus ci
41 34 89.5 1037 2 O8VLQ3 O8VLQ3 alteromonas
42 34 89.5 1322 2 Q6CKZ5 Q6CKZ5 kluyveromyc
43 34 89.5 1635 2 O17412 O17412 aedes aegypt
44 32 84.2 166 2 Q6T220 Q6T220 glycine max
45 32 84.2 166 2 AA513377 AA513377 glycine m

ALIGNMENTS

RESULT 1

Q6Z6G5 PRELIMINARY; PRT; 262 AA.
AC Q6Z6G5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein P0486G03.18.
GN Name=P0486G03.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005002; BAD17213.1; -
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8

DB 233 FAKYNFD 240

RESULT 2

BAD17213 PRELIMINARY; PRT; 262 AA.
ID BAD17213
AC BAD17213;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein P0486G03.18.
GN P0486G03.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC clone:P0486G03.18";
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005002; BAD17213.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;
 Query Match 94.7%; Score 36; DB 2; Length 262;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 233 FAKYNFD 240
 RESULT 3
 OI7419 PRELIMINARY; PRT; 113 AA.
 AC OI7419;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Chitinase (Fragment).
 GN Name=CHT3;
 OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=30069;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=98324849; PubMed=9662472;
 RX de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
 RT "Chitinases are a multi-gene family in Aedes, Anopheles and
 RT Drosophila."
 RL Insect Mol. Biol. 7:233-239(1998).
 DR EMBL; AF026499; AAB81897.1; -;
 DR HSPF; Q13231; ILG2.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR InterPro; IPR001579; Glyco_hydro_18AS.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; PARTIAL.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 13188 MW; 5EA7DCA6B54B4B37 CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 113;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 100 FAKYNFD 107
 RESULT 4
 O48597 PRELIMINARY; PRT; 196 AA.
 AC O48597;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor protein.
 GN Name=CDK1;
 OS Chenopodium rubrum (Red goosefoot) (pigweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Chenopodium.
 OX NCBI_TaxID=3560;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=99329903; PubMed=10409053;
 RX Fountain M.D., Renz A., Beck E.;
 RA "Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor
 RT from suspension-cultured photoautotrophic chenopodium rubrum cells.";
 RL Plant Physiol. 120:339-339(1999).
 DR EMBL; AJ002173; CAA05215.1; -;
 DR PIR; T09968; T09968.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 SQ SEQUENCE 196 AA; 21685 MW; 150349F7ED82A6B2 CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 196;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 171 FSEKYNFD 178
 RESULT 5
 Q8GUA2 PRELIMINARY; PRT; 207 AA.
 ID Q8GUA2;
 AC Q8GUA2;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor.
 GN Name=Kis2;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1] SEQUENCE FROM N.A.
 RP Jasinaki S., Saraiva Leite C., Domenichini S., Stevens R., Raynaud C.,
 RA Perennes C., Bergounioux C., Glab N.;
 RT "Ntkis2, a novel tobacco cyclin-dependent kinase inhibitor
 RT differentially expressed during the cell cycle and plant
 RT development."
 RL Plant Physiol. Biochem. 41:667-676(2003).
 DR EMBL; AJ517183; CAD56868.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a.; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 SQ SEQUENCE 207 AA; 23278 MW; F5AE70AD2261BC2D CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 207;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXKYNFD 8
 DB 180 FTKYNFD 187
 RESULT 6
 Q8EV36 PRELIMINARY; PRT; 442 AA.
 ID Q8EV36;
 AC Q8EV36;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Conserved hypothetical.
 GN OrderedLocusNames=NYPE7310;
 OS Mycoplasma penetrans.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=28227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HF-2;
 RX MEDLINE=22354719; PubMed=12466555;
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 RT intracellular bacterial pathogen in humans."
 RL Nucleic Acids Res. 30:5293-5300(2002).
 DR EMBL: AP041173; BAC44525.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 442 AA; 50767 MW; 240200E4470ED768 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 442;
 Best Local Similarity 75.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 |
 60 FISKYNFD 67

RESULT 7

Q97LUS PRELIMINARY; PRT; 627 AA.
 AC Q97LUS;
 DT 01-OCT-2001 (TREMELrel. 18, Created)
 DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE NtrC family transcriptional regulator (PAS and AAA domains).
 GN OrderedLocNames=CAC0459;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11456286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiti J., Wolf Y.I.,
 RA Tatusev R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RA "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 CC -1- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding
 domain.
 DR EMBL: A3007560; AAK78439.1; -
 DR PIR: D96956; D96956.
 DR GO: GO:000166; F:nucleotide binding; IEA.
 DR GO: GO:0004871; F:signal transducer activity; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:000160; P:two-component signal transduction system (p. .); IEA.
 DR InterPro: IPR001593; AAA_ATPase.
 DR InterPro: IPR009057; Homeodomain-like.
 DR InterPro: IPR02137; HTH_Fis.
 DR InterPro: IPR000014; PAS.
 DR InterPro: IPR010524; Prip_N.
 DR InterPro: IPR02078; Sigs4_interact.
 DR Pfam: PF02954; HTH_8; 1.
 DR Pfam: PF02989; PAS; 1.
 DR Pfam: PF06506; PIPR_N; 1.
 DR Pfam: PF00158; Sigma54_activat; 1.
 DR SMART: SM00382; AAA; 1.
 DR SMART: SM00091; PAS; 1.
 DR TIGRFAMs: TIGR01199; HTH_fis; 1.
 DR TIGRFAMs: TIGR00229; sensory_box; 1.
 DR PROSITE: PS01112; PAS; 1.
 DR PROSITE: PS00675; SIGMA54_INTERACT_1; 1.

DR PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
 DR PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
 KW ATP-binding; Complete proteome; DNA-binding; Transcription regulation.
 SQ SEQUENCE 627 AA; 71062 MW; 4A652FA3AB362ADG CRC64;

Query Match 92.1%; Score 35; DB 2; Length 627;
 Best Local Similarity 75.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 |
 311 FVAKYNFD 318

RESULT 8

Q9QTG7 PRELIMINARY; PRT; 1275 AA.
 AC Q9QTG7;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE NTX (Fragment).
 GN Name=ntx;
 OS Clostridium botulinum D bacteriophage.
 OC Viruses.
 OX NCBI_TaxID=29342;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1873;
 RX MEDLINE=99017546; PubMed=9802560;
 RA Nakajima H., Inoue K., Ikeda T., Fujinaga Y., Sunagawa H., Takeshi K.,
 RA Ohyanaka T., Watanabe T., Inoue K., Oguma K.;
 RT "Molecular composition of the 16S toxin produced by a Clostridium
 RT botulinum type D strain, 1873."
 RL Microbiol. Immunol. 42:599-605(1998).
 DR EMBL: A3012112; BAA75084.1; -
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0003405; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR011591; Botulinum.
 DR InterPro: IPR008985; ConA-like lec_gl.
 DR InterPro: IPR011065; Kunitz-like_M27.
 DR InterPro: IPR000395; Peptidase_M27.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR Pfam: PF01742; Peptidase_M27; 1.
 DR PRINTS: PR00750; BONTOXILYSIN.
 DR ProDom: PD001963; Botulinum; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 FT NON TER 1275 1275
 SQ SEQUENCE 1275 AA; 146742 MW; 3C50F46C8233E2D6 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1275;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
 |
 326 FSEKYNFD 333

RESULT 9

BXD_CLOBO STANDARD; PRT; 1276 AA.
 ID BXD_CLOBO
 AC P19321;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BONT/D)
 DE Bontoxilysin D).
 GN Name=botD;
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.

OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Type D / BVD/-3;
RX MEDLINE=91016853; PubMed=2216736;
RA Binz T., Kurazono H., Popoff M.R., Eklund M.W., Sakaguchi G.,
RA Kozaki S., Krieglstein K., Henschen A., Gill D.M., Niemann H.;
RT "Nucleotide sequence of the gene encoding Clostridium botulinum
RL neurotoxin type D";
RL Nucleic Acids Res. 18:5556-5556(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Type D / CB-16;
RX MEDLINE=93042276; PubMed=1420572;
RA Sunagawa H., Ohyanagi T., Watanabe T., Inoue K.;
RA "The complete amino acid sequence of the Clostridium botulinum type D
RT neurotoxin, deduced by nucleotide sequence analysis of the encoding
RT phase d-16 phi genome.";
RL J. Vet. Med. Sci. 54:905-913(1992).
RN [3]
RP PARTIAL SEQUENCE.
RC STRAIN=Type D / South African, and Type D / D-1873;
RX MEDLINE=89339741; PubMed=2668193;
RA Moriishi K., Syuto B., Kubo S., Oguma K.;
RT "Molecular diversity of neurotoxins from Clostridium botulinum type D
RT strains.";
RL Infect. Immun. 57:2896-2891(1989).
RN [4]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94230352; PubMed=8175689;
RA Yamasaki S., Baumeister A., Binz J., Biasi J., Link E., Cornille F.,
RA Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;
RT "Cleavage of members of the synaptobrevin/VAMP family by types D and F
RT botulin neurotoxins and tetanus toxin.";
RL J. Biol. Chem. 269:12764-12772(1994).
CC -!- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter
CC release. It binds to peripheral neuronal synapses, is internalized
CC and moves by retrograde transport up the axon into the spinal cord
CC where it can move between postsynaptic and presynaptic neurons. It
CC inhibits neurotransmitter release by acting as a zinc
CC endopeptidase that cleaves the 60-Lys-|-Leu-61 bond of
CC synaptobrevins-1 and -2.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C, D, E, F, and G.
CC -!- MISCELLANEOUS: Botulinum type D neurotoxin is synthesized by D
CC strains of C. botulinum which carry the appropriate bacteriophage.
CC -!- SIMILARITY: Belongs to peptidase family M27.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; X54254; CAA38175.1; -;
DR EMBL; S49407; AAB24244.1; -;
DR PIR; S11455; S11455.
DR HSP; P10844; I131.
DR MEROPS; M27.002; -;
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR011065; Kunitz-like.
DR InterPro; IPR000395; Peptidase_M27.

DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOKILYSIN.
DR PRODOM; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin;
KW Transmembrane; Zinc.
FT CHAIN 1 442 Botulinum neurotoxin D light-chain.
FT CHAIN 443 1276 Botulinum neurotoxin D heavy-chain.
FT METAL 229 229 Zinc (catalytic) (By similarity).
FT ACT_SITE 230 230 By similarity.
FT METAL 233 233 Zinc (catalytic) (Probable).
FT DISULFID 437 450 Interchain (Probable).
FT VARIANT 15 16 ND -> PV (in strain D-SA).
FT VARIANT 17 18 ND -> LQ (in strain D-1873).
FT VARIANT 452 452 K -> Q (in strain D-SA).
FT VARIANT 457 457 R -> T (in strain D-SA).
FT VARIANT 457 457 R -> F (in strain D-1873).
FT VARIANT 462 462 A -> D (in strain D-1873).
FT VARIANT 489 489 K -> N (in strain CB16).
FT VARIANT 644 644 N -> K (in strain CB16).
FT VARIANT 1122 1122 Q -> R (in strain CB16).
SQ SEQUENCE 1276 AA; 146871 MW; C1E50F46C8233E2 CRC64;
Query Match 92.1%; Score 35; DB 1; Length 1276;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FXXKYNFD 8
Db 326 FSEKYNFD 333
RESULT 10
Q45967
ID Q45967 PRELIMINARY; PRT; 1285 AA.
AC Q45967;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neurotoxin consisting of botulinum neurotoxin D and C1.
OS Clostridium botulinum D.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=36829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=South African;
RX MEDLINE=96283801; PubMed=8679691;
RA Moriishi K., Koura M., Abe N., Fujii N., Fujinaga Y., Inoue K.,
RA Ogumad K.;
RT "Mosaic structures of neurotoxins produced from Clostridium botulinum
RT types C and D organisms.";
RL Biochim. Biophys. Acta 1307:123-126(1996).
DR EMBL; D38442; BAA07477.1; -;
DR HSP; P10844; I131.
DR MEROPS; M27.002; -;
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR011591; Botulinum.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR011065; Kunitz-like.
DR InterPro; IPR000395; Peptidase_M27.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOKILYSIN.
DR PRODOM; PD001963; Botulinum; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Neurotoxin.
SQ SEQUENCE 1285 AA; 147365 MW; EED898E4EAC6A413 CRC64;
Query Match 92.1%; Score 35; DB 2; Length 1285;

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Best Local Similarity 75.0%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 FXXKYNFD 8
DB 326 FSEKYNFD 333

RESULT 11
Q9LBR1 PRELIMINARY; PRT; 1285 AA.
AC Q9LBR1;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Neurotoxin.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D-4947;
RX MEDLINE=21659747; PubMed=11713244;
RA Kouguchi H., Watanabe T., Sagane Y., Sunagawa H., Ohyama T.;
RT "In vitro reconstruction of the clostridium botulinum type D
progenitor toxin."
RL J. Biol. Chem. 277:2650-2656(2002).
DR EMBL; AB037920; BAA90661.1; -.
DR HSPF; P10844; I131.
DR MEROPS; M27.002; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPRO11591; Botulinum.
DR InterPro; IPRO08985; ConA like lec_gl.
DR InterPro; IPRO11065; Kunitz-like.
DR InterPro; IPRO00395; Peptidase M27.
DR InterPro; IPRO06025; Pept M Zn BS.
DR Pfam; PF01742; Peptidase M27; 1.
DR PRINTS; PR00760; BONTXILYGIN.
DR ProDom; PD001963; Botulinum: 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Neurotoxin.
SQ SEQUENCE 1285 AA; 147351 MW; B63AFA487D570680 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1285;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
DB 326 FSEKYNFD 333

RESULT 12
Q759A3 PRELIMINARY; PRT; 1640 AA.
ID Q759A3
AC Q759A3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE ADR374Cp.
GN Name=ADR374C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,

Best Local Similarity 92.1%; Score 35; DB 2; Length 1640;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavie A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome."
RL Science 304:304-307(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016893; AAS52294.1; -.
DR AGD; ADR374C; -.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006592; RNA_pola_N.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR007080; RNA_pol_Rpb1_1.
DR InterPro; IPR007066; RNA_pol_Rpb1_3.
DR InterPro; IPR007083; RNA_pol_Rpb1_4.
DR InterPro; IPR007081; RNA_pol_Rpb1_5.
DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR SMART; SM00663; RPOLA_N; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
SQ SEQUENCE 1640 AA; 182887 MW; 4B89F52FC18BCDF0 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1640;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXKYNFD 8
DB 1432 FISKYNFD 1439

RESULT 13
AAS52294 PRELIMINARY; PRT; 1640 AA.
ID AAS52294
AC AAS52294;
DT 23-APR-2004 (TRENBLrel. 27, Created)
DT 23-APR-2004 (TRENBLrel. 27, Last sequence update)
DT 23-APR-2004 (TRENBLrel. 27, Last annotation update)
DE ADR374Cp.
GN ADR374C.
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavie A.,
Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome."
RL Science 304:304-307(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016893; AAS52294.1; -.
DR EMBL; AE016893; AAS52294.1; -.
SQ SEQUENCE 1640 AA; 182887 MW; 4B89F52FC18BCDF0 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1640;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 FXXKYNFD 8
Db      1432 FISKYNFD 1439

RESULT 14
Q6FV16 PRELIMINARY; PRT; 1643 AA.
AC Q6FV16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Strain CBS138 chromosome E complete sequence.
GN ORFNames=CAGLOE05500g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380951; CAG58847.1; -
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006592; RNA_dola_N.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR007080; RNA_pol_Rpb1_1.
DR InterPro; IPR007066; RNA_pol_Rpb1_3.
DR InterPro; IPR007083; RNA_pol_Rpb1_4.
DR InterPro; IPR007081; RNA_pol_Rpb1_5.
DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
DR SMART; SMO0663; RPOLA_N; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 1643 AA; 184865 MW; FD2B3ED14021FC18 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1643;
Best Local Similarity 75.0%; Pred.No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
Db      1437 FVTKYNFD 1444

```

```

RESULT 15
Q6CIX4 PRELIMINARY; PRT; 1653 AA.
AC Q6CIX4;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Strain NRRL Y-1140 chromosome F of strain NRRL Y-1140 of Kluyveromyces

```

```

DE lactis.
GN ORFNames=KLLA0F23243g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekaja F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382126; CAG98823.1; -
DR EMBL; CR382126; CAG98823.1; -
SQ SEQUENCE 1653 AA; 185832 MW; E1A9732COAAE8387 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1653;
Best Local Similarity 75.0%; Pred.No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXKYNFD 8
Db      1447 FVTKYNFD 1454

Search completed: October 26, 2004, 15:39:25
Job time : 48.6154 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 44.6154 Seconds
(without alignments)
64.324 Million cell updates/sec

Title: US-09-574-735C-35

Perfect score: 40

Sequence: 1 XLXGRYEW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	8	5	ABG65714 Plant ICK
2	38	95.0	53	5	ABG65677 Loblolly
3	38	95.0	136	3	AY44339 Arabidops
4	38	95.0	137	5	AAE25107 Arabidops
5	38	95.0	216	2	AAW98180 Arabidops
6	38	95.0	222	5	AAE25111 Arabidops
7	38	95.0	222	8	ADN72351 Thale cre
8	37	92.5	8	5	ABG65721 Plant ICK
9	37	92.5	8	5	ABG65712 Plant ICK
10	37	92.5	22	5	ABG65671 OsICK l p
11	37	92.5	38	3	AB26247 Soybean C
12	37	92.5	38	3	AAPO1942 Soybean C
13	37	92.5	87	3	AAPO1951 Cyclin de
14	37	92.5	87	3	AB27253 Soybean c
15	37	92.5	138	2	AY08846 Murine mu
16	37	92.5	138	2	AY08818 Murine p27
17	37	92.5	171	3	AG42859 Arabidops
18	37	92.5	171	3	AG15427 Arabidops
19	37	92.5	183	2	AY08845 Murine mu
20	37	92.5	183	2	AY08840 Murine mu
21	37	92.5	183	2	AY08812 Murine p27
22	37	92.5	183	2	AY08817 Murine p27
23	37	92.5	191	3	AY44335 Arabidops
24	37	92.5	191	3	AG15426 Arabidops
25	37	92.5	191	3	AG42858 Arabidops

ALIGNMENTS

RESULT 1

ABG65714

ID ABG65714 standard; peptide; 8 AA.

XX ABG65714;

DT 27-AUG-2002 (first entry)

DE Plant ICK protein conserved motif 1 #22.

XX Plant; inhibitor of cyclin dependent kinase; ICK.

XX Arabidopsis thaliana.

XX WO200228893-A2.

XX 11-APR-2002.

XX 29-JUN-2001; 2001WO-IB001492.

XX 14-JUL-2000; 2000US-0218471P.

XX 13-OCT-2000; 2000US-0241219P.

XX (CROP-) CROPDESIGN NV.

XX Frankard VMG, Peres Bota AM, Droual A, Mironov V, Inze D;
Hatzfeld Y;

XX WPI; 2002-471311/50.

XX Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide used
to screen substrates, drugs or compounds which modulate ICK activity and
treat disorders characterized by an insufficient or excessive production
of ICK inhibitors.

XX Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated
ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
the invention may be used for treating disorders characterised by
insufficient or excessive production of an ICK inhibitor. The protein of
the invention may also be used to screen for naturally-occurring ICK
substrates, drugs or compounds which modulate ICK activity, as well as to
treat disorders characterised by insufficient or excessive production of
ICK protein, forms which have decreased or aberrant activity compared to
ICK wild type protein. The present sequence represents an inhibitor of
cyclin dependent kinase (ICK) protein of the invention

```

SQ Sequence 8 AA;
  Query Match          95.0%; Score 38; DB 5; Length 8;
  Best Local Similarity 85.7%; Pred. No. 1.7e+06;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
Db 2 LSGRYEW 8
  |||||
  |||||

RESULT 2
ABG65677
ID ABG65677 standard; protein; 53 AA.
XX
AC ABG65677;
XX
DT 27-AUG-2002 (first entry)
XX
DE Loblolly ICK protein.
XX
KW Plant; inhibitor of cyclin dependent kinase; ICK.
XX
OS Pinus taeda.
XX
XX WO200228893-A2.
XX
PD 11-APR-2002.
XX
PF 29-JUN-2001; 2001WO-IB001492.
XX
PR 14-JUL-2000; 2000US-0218471P.
PR 13-OCT-2000; 2000US-0241219P.
XX
PA (CROP-) CROPEDESIGN NV.
XX
PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
PI Hatzfeld Y;
XX
WPI; 2002-471311/50.
XX
Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
PT to screen substrates, drugs or compounds which modulate ICK activity and
PT treat disorders characterized by an insufficient or excessive production
PT of ICK inhibitors.
XX
PS Claim 48; Example 5; 141pp; English.
XX
This invention relates to the DNA and protein sequences of novel isolated
CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
CC the invention may be used for treating disorders characterised by
CC insufficient or excessive production of an ICK inhibitor. The protein of
CC the invention may also be used to screen for naturally-occurring ICK
CC substrates, drugs or compounds which modulate ICK activity, as well as to
CC treat disorders characterised by insufficient or excessive production of
CC ICK protein, forms which have decreased or aberrant activity compared to
CC ICK wild type protein. The present sequence represents an inhibitor of
CC cyclin dependent kinase (ICK) protein of the invention
XX
SQ Sequence 53 AA;
  Query Match          95.0%; Score 38; DB 5; Length 53;
  Best Local Similarity 85.7%; Pred. No. 4.1;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
Db 42 LSGRYEW 48
  |||||
  |||||

RESULT 3
AA44339
ID AAY44339 standard; protein; 136 AA.

XX
AC AAY44339;
XX
DT 29-FEB-2000 (first entry)
XX
DE Arabidopsis thaliana CDK inhibitor, ICN7.
XX
KW Cyclin-Dependent Kinase inhibitor; CDK; Interactor of Cyclin 7; ICN7;
KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility.
XX
OS Unidentified.
XX
PN WO964599-A1.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-CA000532.
XX
PR 08-JUN-1998; 98CA-02235978.
PR 31-DEC-1998; 98CA-02256121.
XX
PA (MIAC ) AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CANA ) NAT RES COUNCIL CANADA.
XX
PI Wang H, Fowke LC, Crosby WL;
XX
WPI; 2000-097540/08.
XX
N-PSDB; AA229419.
XX
Modifying plant cell development using nucleic acid encoding inhibitor of
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
PT inducing male sterility.
XX
PS Disclosure; Fig 7; 58pp; English.
XX
The present protein sequence is ICN7, which inhibits A. thaliana Cyclin-
CC Dependent Kinase (CDK). Interactor of Cyclin 7 (ICN7) interacts with
CC Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and
CC sequence similarity with ICK1. Growth, morphogenesis, multiplication,
CC enlargement, differentiation and maturation of plant cells can be
CC modified by transforming them with nucleic acid encoding CDK inhibitor or
CC antisense construct complementary to the inhibitor gene, operably linked
CC to a tissue-specific promoter. The transgenic plants exhibit alteration
CC of traits such as petals, male sterility and ability to set seeds
XX
SQ Sequence 136 AA;
  Query Match          95.0%; Score 38; DB 3; Length 136;
  Best Local Similarity 85.7%; Pred. No. 11;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
Db 125 LSGRYEW 131
  |||||
  |||||

RESULT 4
AAE25107
ID AAE25107 standard; protein; 137 AA.
XX
AC AAE25107;
XX
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICN7 partial protein.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
KW ICN2; ICN6; ICN7; ICN8; ICK; morphogenesis; maturation; enlargement;
KW plant breeding; growth.
XX

```


OS Arabidopsis thaliana.
 XX WO200250292-A2.
 PN
 XX
 XX
 PD 27-JUN-2002.
 XX
 XX
 PF 18-DEC-2001; 2001WO-CA001825.
 XX
 PR 18-DEC-2000; 2000US-0255908P.
 XX
 XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX
 XX Wang H, Zhou Y, Fowke LC;
 PI
 XX WPI; 2002-519888/55.
 DR N-PSDB; AAD40767.
 DR
 XX
 XX Modifying plant development, e.g. growth or maturation, which is
 PT particularly useful in plant breeding, by introducing nucleic acids
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
 PT that bind to CDK inhibitors.
 XX
 XX Disclosure; Fig 10A; 89pp; English.
 PS
 XX The invention relates to a method for the development of a plant. The
 CC method involves introducing into a plant cell a nucleic acid encoding a
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
 CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and
 CC ICNK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
 CC degradation of a CDK inhibitor polypeptide. The method is useful for
 CC modifying the growth and development of plants e.g. morphogenesis,
 CC growth, multiplication, enlargement, differentiation or maturation of a
 CC cell or plant. It is particularly useful in plant breeding. The present
 CC sequence is A. thaliana ICN7 partial protein
 XX
 SQ Sequence 137 AA;
 Query Match 95.0%; Score 38; DB 5; Length 137;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 Db 126 LSGRYEW 132
 RESULT 5
 AAW98180
 ID AAW98180 standard; protein; 216 AA.
 XX
 XX AAW98180;
 AC
 XX
 XX 05-JUL-1999 (first entry)
 DT
 XX Arabidopsis cyclin-dependent kinase inhibitor FL66.
 DE
 XX Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL66;
 KW plant development; transgenic plant; cell cycle; growth regulator;
 KW herbicide.
 XX
 XX Arabidopsis thaliana.
 OS
 XX
 XX Key Location/Qualifiers
 FH 11..216
 FT Protein /note= "this protein region is specifically claimed in
 FT Claim 1(c)"
 FT
 XX WO9914331-A2.
 PN
 XX 25-MAR-1999.
 PD
 XX
 XX 16-SEP-1998; 98WO-EP005895.
 PF

XX 16-SEP-1997; 97EP-00202838.
 PR 24-DEC-1997; 97EP-00204111.
 XX
 XX (CROP-) CROPDESIGN NV.
 PA
 XX Inze D, De Veylder L, De Almeida J, Landrieu I;
 PI
 XX WPI; 1999-229535/19.
 DR N-PSDB; AAX25016.
 DR
 XX DNA encoding inhibitor of cyclin-dependent kinase.
 PT
 XX Claim 1a; Page 76-77; 89pp; English.
 PS
 XX The present sequence is FL66, a new cyclin-dependent kinase (CDK)
 CC inhibitor of Arabidopsis thaliana encoded by a cDNA clone (see AAX25016)
 CC obtained by two-hybrid screening using CDC2AAT protein as bait. Results
 CC established that several CDK inhibitors (see also AAW98179 and AAW98181)
 CC exist in plants and that these inhibitors are expressed at different time
 CC points and may have different functions during the development of the
 CC plant. CDK inhibitors, nucleic acids, antibodies, promoter sequences,
 CC related recombinant DNA and vectors are all useful: for diagnosis (no
 CC details); for modulating the cycle, division and/or growth of plant cells
 CC ; for altering activity of CDK; for modulating growth inhibition in
 CC plants caused by environmental stress; for inducing male or female
 CC sterility; for altering cell division progression in plants; bacteria,
 CC fungi, insect and animal cells; and to screen for agonists or antagonists
 CC that are potentially useful as growth regulators or herbicides. Plants of
 CC any sort can be treated, e.g. to alter their size or resistance to
 CC disease
 XX
 XX Sequence 216 AA;
 SQ
 Query Match 95.0%; Score 38; DB 2; Length 216;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 Db 205 LSGRYEW 211
 RESULT 6
 AAE25111
 ID AAE25111 standard; protein; 222 AA.
 XX
 XX AAE25111;
 AC
 XX 30-OCT-2002 (first entry)
 DT
 XX Arabidopsis thaliana ICN7 full-length protein.
 DE
 XX Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
 KW ICN2; ICN6; ICN7; ICN8; ICNK; morphogenesis; maturation; enlargement;
 KW plant breeding; growth.
 XX
 XX Arabidopsis thaliana.
 OS
 XX WO200250292-A2.
 PN
 XX 27-JUN-2002.
 PD
 XX 18-DEC-2001; 2001WO-CA001825.
 PF
 XX 18-DEC-2000; 2000US-0255908P.
 PR
 XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX
 XX Wang H, Zhou Y, Fowke LC;
 PI
 XX WPI; 2002-519888/55.
 DR

DR N-PSDB; AAD40771.
 XX
 PT Modifying plant development, e.g. growth or maturation, which is
 PT particularly useful in plant breeding, by introducing nucleic acids
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
 PT that bind to CDK inhibitors.
 XX
 PS Disclosure; Fig 10B; 89pp; English.
 XX
 CC The invention relates to a method for the development of a plant. The
 CC method involves introducing into a plant cell a nucleic acid encoding a
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
 CC inhibitor polypeptide (such as ICK1, ICK2, ICK3, ICK4, ICK5, ICK6, ICK7, ICK8 and
 CC ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
 CC degradation of a CDK inhibitor polypeptide. The method is useful for
 CC modifying the growth and development of plants e.g. morphogenesis,
 CC growth, multiplication, enlargement, differentiation or maturation of a
 CC cell or plant. It is particularly useful in plant breeding. The present
 CC sequence is A. thaliana ICK7 full-length protein
 XX
 SQ Sequence 222 AA;
 Query Match 95.0%; Score 38; DB 5; Length 222;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 211 LSGRYEW 217
 RESULT 7
 ADN72351
 ID ADN72351 standard; protein; 222 AA.
 AC
 XX ADN72351;
 XX
 DT 15-JUL-2004 (first entry)
 DE
 XX Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 246.
 KW plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 KW animal feed product; thale cress; cell wall biosynthesis;
 KW nitrogen metabolism; carbon metabolism.
 XX
 OS Arabidopsis thaliana.
 XX
 FN WO2004035798-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 20-OCT-2003; 2003WO-EP011658.
 XX
 PR 18-OCT-2002; 2002EP-00079408.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Inze D, De Veylder L, Vlieghe K;
 XX
 DR WPI; 2004-348466/32.
 DR N-PSDB; ADN72350.
 XX
 XX Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprising modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX
 PS Claim 1; SEQ ID NO 246; 134pp; English.
 XX
 CC This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to

CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis.
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 CC invention.
 XX
 SQ Sequence 222 AA;
 Query Match 95.0%; Score 38; DB 8; Length 222;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 211 LSGRYEW 217
 RESULT 8
 ABG65721
 ID ABG65721 standard; peptide; 8 AA.
 AC
 XX ABG65721;
 XX
 DT 27-AUG-2002 (first entry)
 DE
 XX Plant ICK protein conserved motif 1 #29.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Oryza sativa.
 XX
 FN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Frankard VMS, Peres Bota AM, Drouau A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 XX
 XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Disclosure; Page 14; 141pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to

CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 SQ Sequence 8 AA;

Query Match 92.5%; Score 37; DB 5; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
 | | | | |
 Db 2 LQGRYEW 8

RESULT 9
 ABG65712
 ID ABG65712 standard; peptide; 8 AA.
 XX
 AC ABG65712;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Plant ICK protein conserved motif 1 #20.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 XX
 PS (CROP-) CROPDESIGN NV.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 PS Disclosure; Page 14; 141pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 SQ Sequence 8 AA;

Query Match 92.5%; Score 37; DB 5; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
 | | | | |
 Db 2 LQGRYEW 8

RESULT 10
 ABG65671
 ID ABG65671 standard; protein; 22 AA.
 XX
 AC ABG65671;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE OsICK 1 protein.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Oryza sativa.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93951.
 XX
 PS Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 CC Claim 48; Fig 4; 141pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 SQ Sequence 22 AA;

Query Match 92.5%; Score 37; DB 5; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
 | | | | |
 Db 11 LQGRYEW 17

RESULT 11
 AAB26247
 ID AAB26247 standard; protein; 38 AA.
 XX
 AC AAB26247;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Soybean cyclin-dependent kinase inhibitor #1.
 XX
 KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
 KW CDKI; cell growth; herbicide.
 XX

OS Glycine max.
 XX WO200060087-A2.
 PN 12-OCT-2000.
 PD 06-APR-2000; 2000WO-US009106.
 XX 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Klein TM, Weng Z, Cahoon RE;
 PI WPI; 2000-679375/66.
 XX N-PSDB; AAA95278.
 DR Cyclin dependent kinase inhibitor sequences, useful for identifying
 XX herbicides and plant growth inhibitors.
 PT Claim 10; Page 42; 58pp; English.
 XX The present sequence is the soybean cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a soybean seedling
 CC cDNA library for sequences similar to those encoding the CDKI from
 CC *Chenopodium rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI
 CC is involved in the cell cycle, and may promote or inhibit cell division
 CC and growth. The protein and its coding sequence are useful in the
 CC production of transgenic plants which produce increased or decreased
 CC amounts of the CDKI protein, in the identification of herbicides, in
 CC genetic and physical mapping and in the isolation of the CDKI gene in
 CC other organisms
 XX
 XX Sequence 38 AA;
 SQ

Query Match 92.5%; Score 37; DB 3; Length 38;
 Best Local Similarity 85.7%; Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 | | | | |
 Db 27 LEGRYEW 33

RESULT 12
 AAP01942
 ID AAP01942 standard; protein; 38 AA.
 AC AAP01942;
 XX 01-NOV-2001 (first entry)
 XX Soybean Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.
 DE Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 XX plant growth inhibitor.
 KW Glycine max.
 XX WO200060087-A2.
 PN 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US009106.
 XX 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Klein TM, Weng Z, Cahoon RE;
 PI WPI; 2000-679375/66.
 XX N-PSDB; AAN02392.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX Claim 10; Page 42; 58pp; English.
 XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the soybean CDKI clone sl2.pk0008.d2 as
 CC described in the method of the invention
 XX
 XX Sequence 38 AA;
 SQ

Query Match 92.5%; Score 37; DB 3; Length 38;
 Best Local Similarity 85.7%; Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 | | | | |
 Db 27 LEGRYEW 33

RESULT 13
 AAP01951
 ID AAP01951 standard; protein; 87 AA.
 XX AAP01951;
 AC 01-NOV-2001 (first entry)
 XX Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2:fls.
 DE Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 XX plant growth inhibitor.
 KW Glycine max.
 XX WO200060087-A2.
 PN 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US009106.
 XX 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Klein TM, Weng Z, Cahoon RE;
 PI WPI; 2000-679375/66.
 XX N-PSDB; AAN02401.
 DR Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX Claim 10; Fig 1; 58pp; English.
 XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the soybean CDKI clone s12.pk0008.d2:fls as
 CC described in the method of the invention
 XX
 XX SQ Sequence 87 AA;

Query Match 92.5%; Score 37; DB 3; Length 87;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LKGRYEW 8
 Db 76 LEGRYEW 82

RESULT 14

AAB27253
 ID AAB27253 standard; protein; 87 AA.

XX AC AAB27253;

XX DT 17-JAN-2001 (first entry)

XX DE Soybean cyclin-dependent kinase inhibitor #2.

XX KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
 XX CDKI; cell growth; herbicide.

XX OS Glycine max.

XX PN WO200060087-A2.

XX PD 12-OCT-2000:

XX PF 06-APR-2000; 2000WO-US009106.

XX PR 07-APR-1999; 98US-0128192P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Klein TM, Weng Z, Cahoon RE;

XX DR WPI; 2000-679375/66.

XX DR N-PSDB; AAA95287.

XX PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 XX herbicides and plant growth inhibitors.

XX PS Claim 10; Fig 1; 58pp; English.

XX CC The present sequence is the soybean cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a soybean seedling
 CC cDNA library for sequences similar to those encoding the CDKI from
 CC Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI
 CC is involved in the cell cycle, and may promote or inhibit cell division
 CC and growth. The protein and its coding sequence are useful in the
 CC production of transgenic plants which produce increased or decreased
 CC amounts of the CDKI protein, in the identification of herbicides, in
 CC genetic and physical mapping and in the isolation of the CDKI gene in
 CC other organisms

XX SQ Sequence 87 AA;

Query Match 92.5%; Score 37; DB 3; Length 87;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LKGRYEW 8

Db 76 LEGRYEW 82

RESULT 15

AAV08846

ID AAV08846 standard; protein; 138 AA.

XX AC AAV08846;

XX DT 13-AUG-1999 (first entry)

XX DE Murine mutant p27 protein from clone #850.

XX KW p163; murine; p27 inhibitor; p27-induced inhibition; cell proliferation;
 XX p27 binding domain; Ran binding domain; detection; screening; malignancy;
 XX tumour; mutant; p27 protein.

XX OS Mus sp.

XX PN EP926236-A1.

XX PD 30-JUN-1999.

XX PF 12-DEC-1998; 98EP-00123708.

XX PR 20-DEC-1997; 97DE-01056975.

XX PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.

XX PI Eilers M, Buergin A, Sedlacek H;

XX DR WPI; 1999-349237/30.

XX PT New p27-inhibiting protein p163 and DNA - useful for detection and/or
 XX quantification of p163 mRNA.

XX PS Disclosure; Page 28; 68pp; German.

XX CC This invention describes (1) a protein that inhibits p27 and thereby
 CC arrests p27-induced inhibition of cell proliferation, (2) the protein of
 CC (1) comprising at least part of the amino acid sequence of murine p163.
 CC (3) a protein that can be derived from the protein of (2) by deletion of
 CC the p27 binding domain or the Ran binding domain, (4) a protein that can
 CC be derived from the protein of (2) by deletion of all amino acid
 CC sequences other than the p27 binding domain, (5) a protein that is the
 CC human or other mammalian species homologue of a protein as in (1)-(4),
 CC (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments
 CC that bind to the p27 binding domain of a protein as above, (8) antibodies
 CC and antibody fragments that bind to the Ran binding domain of a protein
 CC as above, (9) antisense nucleic acids complementary to portions of the
 CC DNA of (6) between codons 121 and 467, (10) a nucleic acid construct
 CC coding for an antisense nucleic acid as in (9) for inhibiting the
 CC proliferation of a cell, in which DNA coding for the antisense nucleic
 CC acid sequence is linked to at least one activation sequence and is
 CC introduced into the target cell as naked DNA or as an insert in a
 CC nonviral or viral vector and (11) a nucleic acid construct containing the
 CC DNA of (6) linked to an activation sequence that permits expression of a
 CC protein as above in a cell. The DNA of (6) can be used for detection
 CC and/or quantification of p163 mRNA in cells and/or tissues, preferably by
 CC Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins
 CC can be used to produce antibodies, which can be used to detect the
 CC corresponding protein in cells, tissues or body fluids. The antisense
 CC nucleic acids can be used to inhibit cell proliferation in vitro or in
 CC vivo. The proteins can be used to screen for substances that inhibit the
 CC interaction between the proteins and their cellular binding partners,
 CC preferably using a two hybrid system or using an affinity system in which
 CC p163 or its p27-binding domain is immobilised on a solid phase, the solid
 CC phase is incubated with a test substance, and the inhibition of the
 CC binding of a labelled binding partner of p163 (especially p27 or Ran) is
 CC measured. Assays for p163 can be used to assess the malignancy of
 CC tumours. This sequence represents a mutant mouse p27 protein sequence
 CC isolated from clone #826 which is used to describe the method of the
 CC invention

XX

SQ Sequence 138 AA;

Query Match 92.5%; Score 37; DB 2; Length 138;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
Db 55 LEGRYEW 61

Search completed: October 26, 2004, 15:36:52
Job time : 45.6154 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds
(without alignments)
40.099 Million cell updates/sec

Title: US-09-574-735C-35

Perfect score: 40

Sequence: 1 XLGRYEW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	222	4	US-09-526-597D-4
2	37	92.5	135	3	US-09-215-221-56
3	37	92.5	180	3	US-09-215-221-50
4	37	92.5	180	3	US-09-215-221-55
5	37	92.5	193	3	US-09-215-221-53
6	37	92.5	194	3	US-09-215-221-51
7	37	92.5	194	3	US-09-215-221-52
8	37	92.5	195	3	US-09-215-221-54
9	37	92.5	197	1	US-08-275-983B-2
10	37	92.5	197	3	US-08-415-655-6
11	37	92.5	197	3	US-09-240-906-8
12	37	92.5	197	3	US-09-215-221-57
13	37	92.5	197	3	US-08-794-002-4
14	37	92.5	197	3	US-08-854-039B-4
15	37	92.5	197	4	US-09-483-597-8
16	37	92.5	197	4	US-08-765-702B-4
17	37	92.5	212	3	US-09-215-221-49
18	37	92.5	355	4	US-09-252-991A-22494
19	36	90.0	223	3	US-09-526-597D-6
20	34	85.0	70	4	US-08-902-572-20
21	34	85.0	80	4	US-09-457-568-18
22	34	85.0	80	4	US-09-457-646-18
23	34	85.0	80	4	US-09-516-065-18
24	34	85.0	167	4	US-08-902-572-18
25	34	85.0	177	4	US-09-457-568-12
26	34	85.0	177	4	US-09-457-646-12
27	34	85.0	177	4	US-09-516-065-12

ALIGNMENTS

RESULT 1

US-09-526-597D-4
; Sequence 4, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-4

Query Match 95.0%; Score 38; DB 4; Length 222;
Best Local Similarity 85.7%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 211 LSGRYEW 217

RESULT 2

US-09-215-221-56
; Sequence 56, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0132
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Murine sp.

Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli

34 85.0 178 3 US-08-794-002-6
34 85.0 178 3 US-08-854-039B-6
34 85.0 178 3 US-08-765-702B-6
34 85.0 198 1 US-08-275-983B-1
34 85.0 198 1 US-08-275-983B-3
34 85.0 198 1 US-08-406-248-4
34 85.0 198 3 US-08-897-333A-2
34 85.0 198 3 US-09-240-906-6
34 85.0 198 3 US-08-794-002-2
34 85.0 198 3 US-08-794-002-22
34 85.0 198 3 US-08-854-039B-2
34 85.0 198 4 US-09-457-568-26
34 85.0 198 4 US-09-457-646-26
34 85.0 198 4 US-09-516-065-26
34 85.0 198 4 US-09-483-597-6
34 85.0 198 4 US-08-765-702B-2
34 85.0 198 4 US-09-378-517B-6
34 85.0 209 4 US-09-526-597D-2

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; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-56

Query Match          92.5%; Score 37; DB 3; Length 135;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 3
US-09-215-221-50
; Sequence 50, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-50

Query Match          92.5%; Score 37; DB 3; Length 180;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 4
US-09-215-221-55
; Sequence 55, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-55

Query Match          92.5%; Score 37; DB 3; Length 180;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      55 LEGRYEW 61

RESULT 5
US-09-215-221-53
; Sequence 53, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-53

Query Match          92.5%; Score 37; DB 3; Length 193;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      65 LEGRYEW 71

RESULT 6
US-09-215-221-51
; Sequence 51, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-51

Query Match          92.5%; Score 37; DB 3; Length 194;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRYEW 8
Db      65 LEGRYEW 71
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Db 66 LEGRYEW 72

RESULT 7

US-09-215-221-52
; Sequence 52, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR FILING DATE: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-52

Query Match 92.5%; Score 37; DB 3; Length 194;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 66 LEGRYEW 72

RESULT 8

US-09-215-221-54
; Sequence 54, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR FILING DATE: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Murine sp.
; FEATURE:
; OTHER INFORMATION: mutated p27
US-09-215-221-54

Query Match 92.5%; Score 37; DB 3; Length 195;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 67 LEGRYEW 73

RESULT 9

US-08-275-983B-2

; Sequence 2, Application US/08275983B
; Patent No. 5688665
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,983B
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,045
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-079CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-275-983B-2

Query Match 92.5%; Score 37; DB 1; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

Db 70 LEGRYEW 76

RESULT 10

US-08-415-655-6
; Sequence 6, Application US/08415655
; Patent No. 6025480
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Lee, Mong-hong
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/415,655
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 1747/47418
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 197 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-415-655-6

Query Match 92.5%; Score 37; DB 3; Length 197;
 Best Local Similarity 85.7%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 Db 70 LEGRYEW 76

RESULT 11
 US-09-240-906-8
 ; Sequence 8, Application US/09240906
 ; Patent No. 6245965
 ; GENERAL INFORMATION:
 ; APPLICANT: ROUSSEL, MARTINE F.
 ; APPLICANT: SWEYNE, RICHARD
 ; APPLICANT: ZINDY, FREDERIQUE
 ; APPLICANT: CUNNINGHAM, JUSTINE
 ; TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 1340-1-025
 ; CURRENT APPLICATION NUMBER: US/09/240,906
 ; CURRENT FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-240-906-8

Query Match 92.5%; Score 37; DB 3; Length 197;
 Best Local Similarity 85.7%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 Db 70 LEGRYEW 76

RESULT 12
 US-09-215-221-57
 ; Sequence 57, Application US/09215221
 ; Patent No. 6265562
 ; GENERAL INFORMATION:
 ; APPLICANT: EILERS, MARTIN
 ; APPLICANT: BUERGIN, ANDREA
 ; APPLICANT: SEDLACEK, HANS-HARALD

; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
 ; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
 ; FILE REFERENCE: 026083/0192
 ; CURRENT APPLICATION NUMBER: US/09/215,221
 ; CURRENT FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 197 56 975.7
 ; PRIOR FILING DATE: 1997-12-20
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 57
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Murine sp.
 ; US-09-215-221-57

Query Match 92.5%; Score 37; DB 3; Length 197;
 Best Local Similarity 85.7%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 Db 70 LEGRYEW 76

RESULT 13
 US-08-794-002-4
 ; Sequence 4, Application US/08794002
 ; Patent No. 6316208
 ; GENERAL INFORMATION:
 ; APPLICANT: Roberts, James M.
 ; APPLICANT: Porter, Peggy L.
 ; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS
 ; TITLE OF INVENTION: PRODUCTION AND USE
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/794,002
 ; FILING DATE: 03-FEB-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: MIV-079.03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 197 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-794-002-4

Query Match 92.5%; Score 37; DB 3; Length 197;
 Best Local Similarity 85.7%; Pred. No. 8.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
 Db 70 LEGRYEW 76

RESULT 14

US-08-854-039B-4
; Sequence 4, Application US/08854039B
; Patent No. 6355774
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS
; TITLE OF INVENTION: PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039B
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-854-039B-4

Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
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Db 70 LEGRYEW 76

RESULT 15

US-09-483-597-8
; Sequence 8, Application US/09483597
; Patent No. 6589505
; GENERAL INFORMATION:
; APPLICANT: ROUSSEL, MARTINE F.
; APPLICANT: SWEYNE, RICHARD
; APPLICANT: ZINDY, FREDERIQUE
; APPLICANT: CUNNINGHAM, JUSTINE
; APPLICANT: SEGIL, NEIL
; APPLICANT: CHEN, PING
; TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-025N
; CURRENT APPLICATION NUMBER: US/09/483,597
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 60/117,719
; EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 115.077 Seconds
(without alignments)
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Title: US-09-574-735c-35

Perfect score: 40

Sequence: 1 XLGRYEW 8

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Searched: 1364641 seqs, 323758627 residues

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Minimum DB seq length: 0

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Maximum Match 100%

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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	53	15	US-10-333-006-17
2	38	95.0	132	16	US-10-767-701-55128
3	38	95.0	137	9	US-09-733-507-4
4	38	95.0	137	15	US-10-451-139-13
5	38	95.0	222	15	US-10-688-291-4
6	38	95.0	222	15	US-10-451-139-21
7	38	95.0	224	15	US-10-424-599-210190
8	37	92.5	22	15	US-10-333-006-11
9	37	92.5	48	15	US-10-424-599-153517
10	37	92.5	191	9	US-09-733-507-2
11	37	92.5	191	9	US-09-733-507-10
12	37	92.5	191	15	US-10-451-139-2
13	37	92.5	197	9	US-09-865-018-4
14	37	92.5	197	9	US-09-865-018-4

14	37	92.5	205	15	US-10-424-599-182928	Sequence 182928,
15	37	92.5	224	16	US-10-437-963-198574	Sequence 198574,
16	37	92.5	235	15	US-10-282-122A-43638	Sequence 43638, A
17	37	92.5	245	13	US-10-087-192-1161	Sequence 1161, Ap
18	36	90.0	95	16	US-10-767-701-36263	Sequence 36263, A
19	36	90.0	205	15	US-10-424-599-235800	Sequence 235800,
20	36	90.0	218	16	US-10-437-963-128205	Sequence 128205,
21	36	90.0	223	15	US-10-688-291-6	Sequence 6, Appli
22	36	90.0	231	15	US-10-282-122A-77900	Sequence 77900, A
23	36	90.0	248	15	US-10-425-114-59718	Sequence 59718, A
24	36	90.0	255	15	US-10-425-114-61054	Sequence 61054, A
25	35	87.5	85	16	US-10-767-701-37255	Sequence 37255, A
26	35	87.5	571	14	US-10-156-761-12275	Sequence 12275, A
27	34	85.0	70	8	US-08-902-572-20	Sequence 20, Appl
28	34	85.0	167	8	US-08-902-572-18	Sequence 18, Appl
29	34	85.0	176	9	US-09-733-507-11	Sequence 11, Appl
30	34	85.0	176	15	US-10-424-599-212181	Sequence 212181,
31	34	85.0	176	15	US-10-451-139-10	Sequence 10, Appl
32	34	85.0	178	9	US-09-865-018-6	Sequence 6, Appli
33	34	85.0	195	15	US-10-451-139-23	Sequence 23, Appl
34	34	85.0	196	9	US-09-733-507-16	Sequence 16, Appl
35	34	85.0	196	15	US-10-451-139-15	Sequence 15, Appl
36	34	85.0	198	9	US-09-865-018-2	Sequence 2, Appli
37	34	85.0	198	10	US-09-970-561-2	Sequence 2, Appli
38	34	85.0	198	13	US-10-087-192-1164	Sequence 1164, Ap
39	34	85.0	198	14	US-10-170-385-303	Sequence 303, App
40	34	85.0	198	14	US-10-458-108-9	Sequence 9, Appli
41	34	85.0	198	15	US-10-302-812-78	Sequence 78, Appl
42	34	85.0	207	15	US-10-451-139-12	Sequence 12, Appl
43	34	85.0	208	9	US-09-733-507-13	Sequence 13, Appl
44	34	85.0	209	15	US-10-688-291-2	Sequence 2, Appli
45	34	85.0	209	15	US-10-451-139-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-333-006-17
; Sequence 17, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Pinus taeda
US-10-333-006-17

Query Match 95.0%; Score 38; DB 15; Length 53;
Best Local Similarity 85.7%; Pred. No. 7.6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;
QY 2 LXGRYEW 8
Db 42 LXGRYEW 48

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RESULT 2
US-10-767-701-55128
; Sequence 55128, Application US/10767701
; Publication No. US2004017284A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55128
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 15724648.pep
US-10-767-701-55128

Query Match          95.0%; Score 38; DB 16; Length 132;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKGRYEW 8
DB      50 LSGRYEW 56

RESULT 3
US-09-733-507-14
; Sequence 14, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada: The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-14

Query Match          95.0%; Score 38; DB 9; Length 137;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKGRYEW 8
DB      126 LSGRYEW 132

RESULT 4
US-10-451-139-13
; Sequence 13, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
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; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255;908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-13

Query Match          95.0%; Score 38; DB 15; Length 137;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKGRYEW 8
DB      126 LSGRYEW 132

RESULT 5
US-10-688-291-4
; Sequence 4, Application US/10688291
; Publication No. US2004007396A1
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/10/688,291
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/526,597D
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-688-291-4

Query Match          95.0%; Score 38; DB 15; Length 222;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKGRYEW 8
DB      211 LSGRYEW 217

RESULT 6
US-10-451-139-21
; Sequence 21, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
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; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-21

Query Match 95.0%; Score 38; DB 15; Length 222;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
DB 211 LSGRYEW 217

RESULT 7
US-10-424-599-210190
; Sequence 210190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210190
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1.pap
US-10-424-599-210190

Query Match 95.0%; Score 38; DB 15; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
DB 213 LSGRYEW 219

RESULT 8
US-10-333-006-11
; Sequence 11, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-11

Query Match 92.5%; Score 37; DB 15; Length 22;
Best Local Similarity 85.7%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
DB 11 LQGRYEW 17

RESULT 9
US-10-424-599-153517
; Sequence 153517, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 153517
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_10964C.1.pap
US-10-424-599-153517

Query Match 92.5%; Score 37; DB 15; Length 48;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
DB 37 LQGRYEW 43

RESULT 10
US-09-733-507-2
; Sequence 2, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependent Kinase Inhibitors as Plant Growth
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-2

Query Match 92.5%; Score 37; DB 9; Length 191;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pap
US-10-424-599-182928

Query Match      92.5%; Score 37; DB 15; Length 205;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LXGRYEW 8
Db 194 LEGRYEW 200

RESULT 15
US-10-437-963-198574
; Sequence 198574, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198574
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9421C.1.pap
US-10-437-963-198574

Query Match      92.5%; Score 37; DB 16; Length 225;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 LXGRYEW 8
Db 203 LQGRYEW 209
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Search completed: October 26, 2004, 15:33:29
Job time : 115.077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds
(without alignments)
69.490 Million cell updates/sec

Title: US-09-574-735C-35
Perfect score: 40
Sequence: 1 XLXGRYEW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	191	2 T01132	cyclin-dependent k
2	37	92.5	197	2 I49064	cyclin-cdk inhibit
3	37	92.5	234	2 C83587	hypothetical prote
4	36	90.0	231	2 A10271	L-ribulose-phospha
5	35	87.5	216	2 A75022	hypothetical prote
6	35	87.5	565	2 T36265	probable uroporphy
7	34	85.0	144	2 T36005	hypothetical prote
8	34	85.0	195	2 H96532	hypothetical prote
9	34	85.0	196	2 T09968	cyclin-dependent k
10	34	85.0	198	2 I52718	gene p27Kip1 prote
11	34	85.0	209	2 T46140	hypothetical prote
12	34	85.0	314	2 G83487	hypothetical prote
13	34	85.0	489	2 S83401	hypothetical prote
14	34	85.0	747	1 QRECFE	ferrichrome-iron r
15	34	85.0	747	2 B85499	outer membrane rec
16	34	85.0	747	2 B90648	outer membrane rec
17	34	85.0	819	2 A13197	TonB-dependent rec
18	34	85.0	880	1 SYBSVS	valine-tRNA ligase
19	34	85.0	888	2 B87270	TonB-dependent rec
20	33	82.5	258	2 T33957	hypothetical prote
21	33	82.5	398	2 A82820	porin O precursor
22	33	82.5	421	2 F83400	hypothetical prote
23	32	80.0	212	2 T18332	icmL protein - Leg
24	32	80.0	292	2 AB0467	phospholipase A [i
25	32	80.0	327	2 T00797	hypothetical prote
26	32	80.0	403	2 B70961	probable esterase
27	32	80.0	461	2 F84676	hypothetical prote
28	32	80.0	466	2 T52061	tRNA isopentenyltr
29	31	77.5	73	2 G95106	hypothetical prote

30 31 77.5 73 2 A97975 hypothetical prote
31 31 77.5 113 2 S40138 T-cell receptor V-
32 31 77.5 131 1 RWHUAA T-cell receptor al
33 31 77.5 144 2 H81823 probable integral
34 31 77.5 146 2 F71263 probable flavodoxi
35 31 77.5 164 2 C82629 hypothethical prote
36 31 77.5 178 2 H86026 hypothethical prote
37 31 77.5 195 2 F91180 hypothethical prote
38 31 77.5 198 2 A82627 hypothethical prote
39 31 77.5 217 1 H71208 hypothethical prote
40 31 77.5 236 2 G82378 hypothethical prote
41 31 77.5 242 2 S47756 lysophospholipase
42 31 77.5 260 2 H84060 lysophospholipase
43 31 77.5 355 2 C70194 probable lipo prot
44 31 77.5 420 2 E70914 gene 10 protein -
45 31 77.5 472 2 S34955

ALIGNMENTS

RESULT 1

T01132
cyclin-dependent kinase inhibitor protein [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F26B6.8
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01132; F84624
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, M.; Koo, H.; Morfat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. M.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.N.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; UID:20083487; PMID:10617197
A;Accession: F84624
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <STO>
A;Cross-references: GB:AE002093; NID:G3242706; PIDN:AAC23758.1; GSPDB:GN00139
C;Genetics:
A;Gene: F26B6.8; At2g23430
A;Map position: 2
A;Introns: 66/73; 81/2; 170/2

Query Match 92.5%; Score 37; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
Db 181 LGRYEW 187

RESULT 2

I49064
cyclin-cdk inhibitor p27 - mouse
N;Alternate names: CDI p27; G1 cyclin-cyclin-dependent kinase inhibitor p27
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: I49064
R;Toyoshima, H.; Hunter, T. Cell 78, 67-74, 1994
A;Title: p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is related to

A;Reference number: A54839; MUID:94306519; PMID:8033213

A;Accession: I49064

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-197 <RES>

A;Cross-references: UNIPROT:P46414; EMBL:U10440; NID:G532771; PIDN:AAA21149.1; PID:G5327

C;Keywords: cell cycle control

Query Match 92.5%; Score 37; DB 2; Length 197;

Best Local Similarity 85.7%; Pred. No. 3.8; 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 70 LGRYEW 76

RESULT 3

C83587

hypothetical protein PA0462 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: C83587

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A;Reference number: A82950; MUID:2043737; PMID:10984043

A;Accession: C83587

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-234 <STO>

A;Cross-references: UNIPROT:Q91656; GB:AE004484; GB:AE004091; NID:G9946320; PIDN:AA0385

A;Experimental source: strain PAO1

C;Genetics:

A;Gene: PA0462

Query Match 92.5%; Score 37; DB 2; Length 234;

Best Local Similarity 85.7%; Pred. No. 4.5;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 87 LYGRYEW 93

RESULT 4

AI0271

L-ribulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AI0271

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AI0271

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-231 <KUR>

A;Cross-references: UNIPROT:Q82EE3; GB:AL590842; PIDN:CAC91037.1; PID:G15980231; GSPDB:G

A;Gene: araD

C;Superfamily: L-ribulose-phosphate 4-epimerase

C;Keywords: isomerase

Query Match 90.0%; Score 36; DB 2; Length 231;

Best Local Similarity 71.4%; Pred. No. 7;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 137 IAGRYEW 143

RESULT 5

A75022

hypothetical protein PAB1224 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: A75022

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Accession: A75022

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-216 <KAW>

A;Cross-references: UNIPROT:Q9UXZ7; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB5061

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB1224

C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

Query Match 87.5%; Score 35; DB 2; Length 216;

Best Local Similarity 71.4%; Pred. No. 10;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 53 MGRYEW 59

RESULT 6

T36265

probable uroporphyrin-III C-methyltransferase / uroporphyrinogen-III synthase - Streptom

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T36265

R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A;Reference number: Z21576

A;Accession: T36265

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-565 <MUR>

A;Cross-references: UNIPROT:Q9WX17; EMBL:AL079345; PIDN:CAB45351.1; GSPDB:GN00070; SCOE

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOE68.15C

C;Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III sy

Query Match 87.5%; Score 35; DB 2; Length 565;

Best Local Similarity 71.4%; Pred. No. 28;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8

DB 334 VTGRYEW 340

RESULT 7

T36005

hypothetical protein SCC22.15c - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T36005

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A;Reference number: Z21574

A;Accession: T36005

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-144 <SEE>
A:Cross-references: UNIPROT:Q9XAC3; EMBL:AL096839; PIDN:CAB50758.1; GSPDB:GN000070; SCOPB:1.114
A:Experimental source: strain A3(2)
C:Genetics:
C:Superfamily: Streptomyces coelicolor hypothetical protein SCC22.15c

Query Match 85.0%; Score 34; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GRVYEW 8
| | | | |
DB 126 GRVYEW 130

RESULT 8
H96532
hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96532
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Holt, T.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Hirsch, N.F.; Hughes, B.; Huizar, L.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Miao, J.; Rooney, T.; Rowley, D.; Sakano, H.; Schaefer, S.; Salzman, S.; Schwan, J.; Schwart, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, B.; Thaler, L.; Wang, D.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:g10120423; PIDN:AAG13048.1; GSPDB:G14J22.14
C:Genetics:
A:Map position: 1

Query Match 85.0%; Score 34; DB 2; Length 195;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
| | | | |
DB 184 LKGRYEW 190

RESULT 9
T09968
cyclin-dependent kinase inhibitor protein - red goosefoot
C:Species: Chenopodium rubrum (red goosefoot)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09968
R:Pountain, M.D.; Renz, A.; Beck, E.
Submitted to the EMBL Data Library, November 1997
A:Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic
A:Reference number: Z16910
A:Accession: T09968
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-196 <FOU>
A:Cross-references: UNIPROT:Q48537; EMBL:AJ002173
A:Experimental source: photoautotrophic cells derived from hypocotyl tissue
C:Genetics:
A:Gene: CDK11
C:Keywords: protein kinase inhibitor

Query Match 85.0%; Score 34; DB 2; Length 196;

Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
| | | | |
DB 185 LKGRYEW 191

RESULT 10
I52718
Gene p27Kip1 protein - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I52718
R:Fiorenza, J.A.; Bohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.; Cancer Res. 55, 1206-1210, 1995
A:Title: Assignment of the human p27Kip1 gene to 12p13 and its analysis in leukemias.
A:Reference number: I52718; MUID:95188144; PMID:7882309
A:Accession: I52718
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-198 <RES>
A:Cross-references: UNIPROT:Q96T50; GB:S76988; NID:g998402; PIDN:AAD14244.1; PID:g42619
C:Genetics:
A:Gene: p27Kip1
A:Introns: 159/1

Query Match 85.0%; Score 34; DB 2; Length 198;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
| | | | |
DB 70 LKGRYEW 76

RESULT 11
T46140
hypothetical protein T3A5.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46140
R:Blöcker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quettier, F.; Sal. submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23024
A:Accession: T46140
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-209 <ELO>
A:Cross-references: UNIPROT:Q9SCR2; EMBL:AL132979
A:Experimental source: cultivar Columbia; BAC clone T3A5
C:Genetics:
A:Map position: 3
A:Introns: 109/3; 130/2; 186/2
A:Note: T3A5.10

Query Match 85.0%; Score 34; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GRVYEW 8
| | | | |
DB 200 GRVYEW 204

RESULT 12
G83487
hypothetical protein PA1268 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83487
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Lim adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim

```

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83487
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:P06971; GB:AE004556; GB:AE004091; NID:G9947194; PIDN:AAG0465
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1268
C;Superfamily: proline racemase

Query Match      85.0%; Score 34; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GRVYEW 8
DB      271 GRVYEW 275

RESULT 13
S63401
hypothetical protein YNR069c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3555
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63401
R;Duesterhoeft, A.; Fliceth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62944
A;Accession: S63401
A;Molecule type: DNA
A;Residues: 1-489 <DUE>
A;Cross-references: UNIPROT:P53755; EMBL:Z71684; NID:G1302601; PID:e239850; PID:G1302602
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR069c
A;Cross-references: SGD:S0005352
A;Map position: 14R

Query Match      85.0%; Score 34; DB 2; Length 489;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRVYEW 8
DB      467 LRGRVYEW 473

RESULT 14
QSECFE
ferrichrome-iron receptor precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: F64738; S25196; S45219; S06358
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64738
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-747 <BLAT>
A;Cross-references: UNIPROT:P06971; GB:AE000124; GB:U00096; NID:G1786339; PIDN:AAC73261.
A;Experimental source: strain K-12, substrain W61655
R;Coulton, J.W.; Mason, P.; Cameron, D.R.; Carmel, G.; Jean, R.; Rode, H.N.
J. Bacteriol. 165, 181-192, 1986
A;Title: Protein fusions of beta-galactosidase to the ferrichrome-iron receptor of Esche
A;Reference number: A25196; MUID:86085668; PMID:3079747

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A;Accession: A25196
A;Molecule type: DNA
A;Residues: 1-608; Rp', 611-747 <COU>
A;Cross-references: GB:D26562; NID:G473770; PIDN:BAA05598.1; PID:G473809
A;Experimental source: strain K-12
R;Fujita, N.
submitted to the EMBL Data Library, January 1994
A;Reference number: S45181
A;Accession: S45219
A;Molecule type: DNA
A;Residues: 1-608; Rp', 611-747 <FUJ>
A;Cross-references: EMBL:D26562; NID:G473770; PIDN:BAA05598.1; PID:G473809
A;Experimental source: strain K-12, substrain W3110
R;Burkhardt, R.; Braun, V.
Mol. Gen. Genet. 209, 49-55, 1987
A;Title: Nucleotide sequence of the fhvC and fhvD genes involved in iron (III) hydroxama
A;Reference number: A32650; MUID:88038363; PMID:2823072
A;Accession: S06358
A;Molecule type: DNA
A;Residues: 723-747 <BUR>
A;Cross-references: EMBL:X05810
C;Genetics:
A;Gene: fhvA; tonA
A;Map position: 4 min
C;Function:
A;Description: located in the outer membrane, binds the ferrichrome-iron ligand; interac
system
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
C;Keywords: iron transport; membrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-747/Product: ferrichrome-iron receptor #status predicted <MAT>
F;98-235/Domain: tonB-dependent receptor amino-terminal homolog <TNN>
F;468-747/Domain: tonB-dependent receptor carboxyl-terminal homolog <TNC>

Query Match      85.0%; Score 34; DB 1; Length 747;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRVYEW 8
DB      482 LGGRYDW 488

RESULT 15
B85499
outer membrane receptor protein FhuA fhuA [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85499
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, A.; Dimalanta, E.; Potamouasis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-747 <STO>
A;Cross-references: UNIPROT:O8X901; GB:AE005174; NID:G12512871; PIDN:AAG54454.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: fhuA
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog

Query Match      85.0%; Score 34; DB 2; Length 747;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LXGRVYEW 8
DB      482 LGGRYDW 488

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Wed Oct 27 09:35:40 2004

Search completed: October 26, 2004, 15:40:08
Job time : 13.0769 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 44.6154 Seconds
(without alignments)
103.171 Million cell updates/sec

Title: US-09-574-735c-35
Perfect score: 40
Sequence: 1 XLXGRYEW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	185	2 Q8GT28	Q8GT28 lycopersico
2	38	95.0	222	2 Q9FKB5	Q9FKB5 arabidopsis
3	37	92.5	163	2 Q93V92	Q93V92 nicotiana t
4	37	92.5	166	2 Q6T220	Q6T220 glycine max
5	37	92.5	166	2 AAS13377	AAS13377 glycine m
6	37	92.5	180	2 Q6T221	Q6T221 glycine max
7	37	92.5	180	2 AAS13376	AAS13376 glycine m
8	37	92.5	191	2 O04154	O04154 arabidopsis
9	37	92.5	191	2 O82809	O82809 arabidopsis
10	37	92.5	191	2 Q8LXD1	Q8LXD1 arabidopsis
11	37	92.5	192	2 Q9FS28	Q9FS28 pisum sativ
12	37	92.5	197	1 CDNB_MOUSE	P46414 mus musculu
13	37	92.5	197	2 O03769	O03769 rattus norv
14	37	92.5	197	2 Q35792	Q35792 rattus norv
15	37	92.5	197	2 Q8BG74	Q8BG74 m mus muscu
16	37	92.5	198	2 Q6T222	Q6T222 glycine max
17	37	92.5	198	2 Q6QWC3	Q6QWC3 anas platyr
18	37	92.5	198	2 Q8JIV2	Q8JIV2 gallus gall
19	37	92.5	198	2 AAS02099	AAS02099 anas plat
20	37	92.5	198	2 AAS13375	AAS13375 glycine m
21	37	92.5	205	2 Q6T223	Q6T223 glycine max
22	37	92.5	205	2 AAS13374	AAS13374 glycine m
23	37	92.5	234	2 Q91656	Q91656 pseudomonas
24	37	92.5	1063	2 Q8BJR3	Q8BJR3 synecococc
25	36	90.0	189	2 Q9LRY0	Q9LRY0 arabidopsis
26	36	90.0	210	2 Q8GT29	Q8GT29 lycopersico
27	36	90.0	231	2 Q8ZEE3	Q8ZEE3 versinia pe
28	36	90.0	267	2 Q8D0J2	Q8D0J2 versinia pe
29	36	90.0	267	2 AAS62245	AAS62245 versinia
30	36	90.0	403	2 Q9CN07	Q9CN07 pasteurella
31	35	87.5	160	2 Q6PV56	Q6PV56 versinia ru

32 35 87.5 160 2 AAS89651
33 35 87.5 216 2 Q9UXZ7-
34 35 87.5 231 2 Q6D5T0
35 35 87.5 565 2 Q9WX17
36 35 87.5 571 2 Q82E75
37 34 85.0 43 2 Q82E75
38 34 85.0 104 2 Q82E75
39 34 85.0 136 2 Q708J1
40 34 85.0 136 2 CAE82383
41 34 85.0 144 2 Q9XAC3
42 34 85.0 156 2 Q93YF6
43 34 85.0 158 2 Q43806
44 34 85.0 172 2 Q9BEA5
45 34 85.0 178 1 CDNB_MUSVI

ALIGNMENTS

RESULT 1

Q8GT28 PRELIMINARY; PRT; 185 AA.
ID Q8GT28
AC Q8GT28; 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P27KIP1-related-protein 2.
GN Name=krp2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamnids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Local;
RA Babis B., Joubes J., Hernould M., Inze D., Raymond P., Chevalier C.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ441250; CAD29649.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 185 AA; 21189 MW; 48DCC89A5336C676 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 185;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 174 LSGRYEW 180

RESULT 2

Q9FKB5 PRELIMINARY; PRT; 222 AA.
ID Q9FKB5
AC Q9FKB5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24G6
DE (Cyclin-dependent kinase inhibitor 3).
GN Name=krp3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98403884; PubMed=9734815;

RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and PAC clones.",
 RL DNA Res. 5:203-216(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21342510; PubMed=11449057;
 RA de Veylder L., Beckman T., Beemster G.T.S., Kroes L., Terras F.,
 RA Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.,
 RT "Functional analysis of Cyclin-dependent kinase inhibitors of
 RT Arabidopsis.",
 RL Plant Cell 13:1653-1668(2001).
 DR EMBL; AB012442; BAB09435.1; -.
 DR EMBL; AJ301554; CAC41617.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0018301; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 222 AA; 24925 MW; 7A3EB2C9A29688A7 CRC64;
 Query Match 95.0%; Score 38; DB 2; Length 222;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 211 LSGRYEW 217
 RESULT 3
 Q93V92 PRELIMINARY; PRT; 163 AA.
 AC Q93V92;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CDK/cyclin inhibitor.
 GN Name=kisla; Synonyms=kisl1;
 OS Nicotiana tomentosiformis (Tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4098;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=23369088; PubMed=12481070;
 RA Jasinski S., Perennes C., Bergounioux C., Glab N.;
 RT "Comparative Molecular and Functional Analyses of the Tobacco Cyclin-
 RT dependent kinase inhibitor Nek1a and its spliced variant NtKIS1b.",
 RL Plant Physiol. 130:1871-1882(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Grondard S.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ297906; CAC82733.1; -.
 DR EMBL; AJ297904; CAC82731.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin.
 SQ SEQUENCE 163 AA; 18301 MW; E154A59D491B66B7 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 163;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 157 LSGRYEW 163
 RESULT 4
 Q6T220 PRELIMINARY; PRT; 166 AA.
 AC Q6T220;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Li S., Reverdatto S., Nielsen N.C.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV439104; AAS13377.1; -.
 DR GO; GO:0016301; P:kinase activity; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 FT NON TER 166
 SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 166;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 157 LSGRYEW 163
 RESULT 5
 AAS13377 PRELIMINARY; PRT; 166 AA.
 AC AAS13377;
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Li S., Reverdatto S., Nielsen N.C.;
 RL "cDNA of cell-cycle genes in soybean cotyledons.",
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV439104; AAS13377.1; -.
 KW Cyclin; Kinase.
 FT NON TER 166
 SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 166;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 157 LSGRYEW 163
 RESULT 6
 Q6T221

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ID Q6T2Z1 PRELIMINARY; PRT; 180 AA.
AC Q6T2Z1.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 2;1 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY439103; AAS13376.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
FT NON_TER 180
SQ SEQUENCE 180 AA; 20060 MW; 9E4ABBF0918246E7 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 180;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
DB 171 LEGRYEW 177

RESULT 7
AAS13376 PRELIMINARY; PRT; 180 AA.
ID AAS13376
AC AAS13376;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 2;1 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RL "cDNA of cell-cycle genes in soybean cotyledons.";
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY439103; AAS13376.1; -.
KW Cyclin; Kinase.
FT NON_TER 180
SQ SEQUENCE 180 AA; 20060 MW; 9E4ABBF0918246E7 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 180;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
DB 171 LEGRYEW 177

RESULT 8
O04154 PRELIMINARY; PRT; 191 AA.
ID O04154
AC O04154;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor protein.
GN Name=ICK1;

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```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang H., Fowke L.C., Crosby W.L.;
RL MEDLINE=97242401; PubMed=9087400;
RT "A plant cyclin-dependent kinase inhibitor gene.";
RL Nature 386:451-452(1997).
DR EMBL; U94772; AAC49698.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 191 AA; 22239 MW; 0432BD4F626C07B5 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKGRYEW 8
DB 181 LEGRYEW 187

RESULT 9
O82809 PRELIMINARY; PRT; 191 AA.
ID O82809
AC O82809;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor.
GN Name=ICK1; Synonyms=Atg23430;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang H., Qi Q., Schorr P., Cutler A.J., Crosby W.L., Fowke L.C.;
RT "ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis
thaliana interacts with both Cdc2a and CycD3, and its expression is
induced by abscisic acid.";
RL Plant J. 15:501-510(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003040; AAC23758.1; -.
DR EMBL; AF079587; AAC34660.1; -.
DR F01; T01132; T01132.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.

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KW Cyclin; Kinase
SQ SEQUENCE 191 AA; 22283 MW; 0477A91E277C46B2 CRC64;
Query Match 92.5%; Score 37; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 LXGRYEW 8
Db 181 LEGRYEW 187
RESULT 10
Q8LXD1 PRELIMINARY; PRT; 191 AA.
AC Q8LXD1; 1
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2208475; PubMed=12093376;
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Broxer V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY085749; AAM62967.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 191 AA; 22282 MW; 19B7A91E277C46B2 CRC64;
Query Match 92.5%; Score 37; DB 2; Length 191;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 LXGRYEW 8
Db 181 LEGRYEW 187
RESULT 11
Q9FS28 PRELIMINARY; PRT; 192 AA.
AC Q9FS28;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cyclin dependent kinase inhibitor.
GN Name=cki;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Axillary bud;
RA Shimizu-Sato S., Mori H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029483; BAB20860.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 192 AA; 21921 MW; E76D73400085EB2 CRC64;
Query Match 92.5%; Score 37; DB 2; Length 192;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 LXGRYEW 8
Db 181 LEGRYEW 187
RESULT 12
CDNB_MOUSE
ID_CDNB_MOUSE STANDARD; PRT; 197 AA.
AC P46414;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin-dependent kinase inhibitor 1B (Cyclin-dependent kinase
DE inhibitor p27) (p27Kip1).
GN Name=Cdkn1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94306519; PubMed=8033213;
RA Toyoshima H., Hunter T.;
RT "p27, a novel inhibitor of G1 cyclin-Cdk protein kinase activity, is
RT related to p21."
RL Cell 78:67-74 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94306518; PubMed=8033212;
RA Polyak K., Lee M.-H., Eddington-Bromage H., Koff A., Roberts J.M.,
RA Tempest P., Massague J.;
RT "Cloning of p27Kip1, a cyclin-dependent kinase inhibitor and a
RT potential mediator of extracellular antimitogenic signals."
RL Cell 78:59-66 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP INTERACTION WITH NUP50, AND MUTAGENESIS.
 RC STRAIN=BAUB/c;
 RX MEDLINE=20271857; PubMed=10811608;
 RA Mueller D., Thieke K., Buerger A., Dickmanns A., Eilers M.;
 RT "Cyclin E-mediated elimination of p27 requires its interaction with
 RL the nuclear pore-associated protein mNUP60.";
 RL EMBO J. 19:2158-2180 (2000).
 CC -|- FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1
 CC arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 CC cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 CC NUP50 is required for nuclear import and for degradation of
 CC phosphorylated p27Kip1 after nuclear import.
 CC -|- SUBUNIT: Interacts with NUP50.
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- SIMILARITY: Belongs to the CDI family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U10440; AAB21149.1; -;
 DR EMBL; U09968; AAA20235.1; -;
 DR EMBL; BC014296; AAB14296.1; -;
 DR EMBL; I49064; I49064.
 DR HSP; P46527; IJUSU.
 DR MGI; MGI:104565; Cdkn1b.
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007050; P:cell cycle arrest; IDA.
 DR GO; GO:0045736; P:negative regulation of CDK activity; IDA.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; IMP.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cell cycle; Nuclear protein; Protein kinase inhibitor.
 KW Cell cycle; Nuclear localization signal (Potential).
 FT DOMAIN 153 169 Nuclear localization signal (Potential).
 FT MUTAGEN 90 90 R->G: Loss of interaction with NUP50.
 SQ SEQUENCE 197 AA; 22210 MW; 2D19A6CF86AE650D CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 197;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 70 LEGRYEW 76
 RESULT 13
 ID C08769 PRELIMINARY; PRT; 197 AA.
 AC C08769;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE p27 kipi (Cyclin kinase inhibitor) (Cyclin dependent kinase
 DE inhibitor).
 GN Name=p27Kip1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawada M., Yamagoe S., Murakami Y., Suzuki K., Mizuno S., Uehara Y.;
 RT "Induction of p27Kip1 degradation and anchorage independence by Ras

RT through the MAP kinase signaling pathway.";
 RL Oncogene 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Uehara Y.; (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Dastvan F., Reidy M.A.;
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Iwanaga R., Komori H., Ohtani K.;
 RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; D86924; BAA19960.1; -;
 DR EMBL; AF015194; AAB71368.1; -;
 DR EMBL; AV623024; AAT46041.1; -;
 DR EMBL; AV623040; AAT46051.1; -;
 DR HSP; P46527; IJUSU.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 KW Cyclin; Kinase.
 SQ SEQUENCE 197 AA; 22139 MW; 55738078C2C9847F CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 70 LEGRYEW 76
 RESULT 14
 ID C05792 PRELIMINARY; PRT; 197 AA.
 AC C05792;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P27.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RX MEDLINE=97381761; PubMed=9218722;
 RA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
 RT "Cloning and characterization of rat p27Kip1, a cyclin-dependent
 RT kinase inhibitor.";
 RL Gene 191:211-218 (1997).
 DR EMBL; D83792; BAA21561.1; -;
 DR HSP; P46527; IJUSU.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR SEQUENCE 197 AA; 22112 MW; 55738078C2D555B2 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LXGRYEW 8
 DB 70 LEGRYEW 76

RESULT 15
QB8G74
ID QB8G74 PRELIMINARY; PRT; 197 AA.
AC QB8G74;
DT 01-WAR-2003 (TRENBLrel. 23, Created)
DT 01-WAR-2003 (TRENBLrel. 23, Last annotation update)
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
DE enriched library, clone:B430307G09 product:cyclin-dependent kinase
DE inhibitor 1B (P27), full insert sequence (Mus musculus adult male
DE corpus striatum cDNA, RIKEN full-length enriched library.
DE clone:CG30007H22 product:cyclin-dependent kinase inhibitor 1B (P27),
DE full insert sequence) (Mus musculus adult male liver tumor cDNA, RIKEN
DE full-length enriched library, clone:C730029L05 product:cyclin-
DE dependent kinase inhibitor 1B (P27), full insert sequence).
GN Name=Cdkn1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,776 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=20530913; PubMed=11078861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose, Corpus striatum, and Liver;
RX MEDLINE=20530913; PubMed=11078861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK046676; BAC32833.1; -;
DR EMBL; AK047669; BAC33119.1; -;
DR EMBL; AK050240; BAC34141.1; -;
DR HSSP; P46527; 1JSU.
DR WGD; MG1:104565; Cdkn1b.
DR GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a. . . ; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007050; P:cell cycle arrest; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IMP.
DR GO; GO:0045736; P:negative regulation of cyclin dependent pro. . . ; IDA.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IMP.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 197 AA; 22193 MW; BAC30D648B9BA3D6 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 197;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXGRYEW 8
| | | | |
Db 70 LEGRYEW 76

Search completed: October 26, 2004, 15:39:27
Job time : 46.6154 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 55.7692 Seconds
(without alignments)
64.324 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFPXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	81.2	10	5	Abg65743 Plant ICK
2	26	81.2	10	5	Abg65738 Plant ICK
3	26	81.2	10	5	Abg65737 Plant ICK
4	26	81.2	87	5	Abg65672 OsICK 3 p
5	26	81.2	108	5	Abg65676 Broom cor
6	26	81.2	262	5	Abg65670 OsICK 2 p
7	25	78.1	10	5	Abg65733 Plant ICK
8	25	78.1	10	5	Abg65739 Plant ICK
9	25	78.1	46	3	AbA26246 Rice cycl
10	25	78.1	46	3	AbP01941 Rice cycl
11	25	78.1	60	3	AbP01953 Cyclin de
12	25	78.1	60	3	Ab27255 Soybean c
13	25	78.1	90	5	Abg65673 Rice Os I
14	25	78.1	99	3	Ab27251 Rice cycl
15	25	78.1	99	3	AbP01949 Cyclin de
16	25	78.1	194	5	Abg65691 Rice OsIC
17	25	78.1	205	3	AbP01952 Cyclin de
18	25	78.1	205	3	AbA27254 Soybean c
19	25	78.1	312	5	Ab28321 Streptoco
20	25	78.1	436	5	AbP30085 Streptoco
21	24	75.0	10	5	Abg65736 Plant ICK
22	24	75.0	10	5	Abg65731 Plant ICK
23	24	75.0	53	5	Abg65677 Lolololy
24	24	75.0	87	3	AbP01951 Cyclin de
25	24	75.0	87	3	AbA27253 Soybean c

ALIGNMENTS

RESULT 1

ABG65743

ID ABG65743 standard; peptide; 10 AA.

XX AC ABG65743;

XX AC

XX 27-AUG-2002 (first entry)

XX XX

DE Plant ICK protein conserved motif 1 #51.

XX XX

KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Sorghum bicolor.

XX XX

XX WO200228893-A2.

XX PD 11-APR-2002.

XX XX

XX 29-JUN-2001; 2001WO-1B001492.

XX PR 14-JUL-2000; 2000US-0218471P.

XX PR 13-OCT-2000; 2000US-0241219P.

XX XX (CROP-) CROPDESIGN NV.

XX PA Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX PI Hatzfeld Y;

XX XX

XX WPI; 2002-471311/50.

XX XX

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

XX PT to screen substrates, drugs or compounds which modulate ICK activity and

XX PT treat disorders characterized by an insufficient or excessive production

XX PT of ICK inhibitors.

XX XX

XX Disclosure; Page 14; 141pp; English.

XX XX

XX This invention relates to the DNA and protein sequences of novel isolated

XX CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of

XX CC the invention may be used for treating disorders characterised by

XX CC insufficient or excessive production of an ICK inhibitor. The protein of

XX CC the invention may also be used to screen for naturally-occurring ICK

XX CC substrates, drugs or compounds which modulate ICK activity, as well as to

XX CC treat disorders characterised by insufficient or excessive production of

XX CC ICK protein, forms which have decreased or aberrant activity compared to

XX CC ICK wild type protein. The present sequence represents an inhibitor of

XX CC cyclin dependent kinase (ICK) protein of the invention

XX XX

XX

```

SQ      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEFPFXXE 10
Db      1 EIEAFFAAE 10

RESULT 2
ABG65738
ID      ABG65738 standard; peptide; 10 AA.
XX      AC
XX      AC ABG65738;
XX      DT 27-AUG-2002 (first entry)
XX      DE Plant ICK protein conserved motif 1 #46.
XX      KW Plant; inhibitor of cyclin dependent kinase; ICK.
XX      OS Oryza sativa.
XX      PN WO200228893-A2.
XX      PD 11-APR-2002.
XX      PF 29-JUN-2001; 2001WO-IB001492.
XX      PR 14-JUL-2000; 2000US-0218471P.
XX      PR 13-OCT-2000; 2000US-0241219P.
XX      PA (CROP-) CROPDESIGN NV.
XX      PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      PI Hatzfeld Y;
XX      OS Oryza sativa.
XX      PN WO200228893-A2.
XX      PD 11-APR-2002.
XX      PF 29-JUN-2001; 2001WO-IB001492.
XX      PR 14-JUL-2000; 2000US-0218471P.
XX      PR 13-OCT-2000; 2000US-0241219P.
XX      PA (CROP-) CROPDESIGN NV.
XX      PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      PI Hatzfeld Y;
XX      DR WPI; 2002-471311/50.
XX      PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX      PT to screen substrates, drugs or compounds which modulate ICK activity and
XX      PT treat disorders characterized by an insufficient or excessive production
XX      PT of ICK inhibitors.
XX      PS Disclosure; Page 14; 141pp; English.
XX      CC This invention relates to the DNA and protein sequences of novel isolated
XX      CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX      CC the invention may be used for treating disorders characterised by
XX      CC insufficient or excessive production of an ICK inhibitor. The protein of
XX      CC the invention may also be used to screen for naturally-occurring ICK
XX      CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX      CC treat disorders characterised by insufficient or excessive production of
XX      CC ICK protein, forms which have decreased or aberrant activity compared to
XX      CC ICK wild type protein. The present sequence represents an inhibitor of
XX      CC cyclin dependent kinase (ICK) protein of the invention
XX      SQ      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEFPFXXE 10
Db      1 EIEAFFAAE 10

RESULT 3
ABG65737
ID      ABG65737 standard; peptide; 10 AA.
XX      AC
XX      AC ABG65737;
XX      DT 27-AUG-2002 (first entry)
XX      DE Plant ICK protein conserved motif 1 #45.
XX      KW Plant; inhibitor of cyclin dependent kinase; ICK.
XX      OS Oryza sativa.
XX      PN WO200228893-A2.
XX      PD 11-APR-2002.
XX      PF 29-JUN-2001; 2001WO-IB001492.
XX      PR 14-JUL-2000; 2000US-0218471P.
XX      PR 13-OCT-2000; 2000US-0241219P.
XX      PA (CROP-) CROPDESIGN NV.
XX      PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX      PI Hatzfeld Y;
XX      DR WPI; 2002-471311/50.
XX      PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX      PT to screen substrates, drugs or compounds which modulate ICK activity and
XX      PT treat disorders characterized by an insufficient or excessive production
XX      PT of ICK inhibitors.
XX      PS Disclosure; Page 14; 141pp; English.
XX      CC This invention relates to the DNA and protein sequences of novel isolated
XX      CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX      CC the invention may be used for treating disorders characterised by
XX      CC insufficient or excessive production of an ICK inhibitor. The protein of
XX      CC the invention may also be used to screen for naturally-occurring ICK
XX      CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX      CC treat disorders characterised by insufficient or excessive production of
XX      CC ICK protein, forms which have decreased or aberrant activity compared to
XX      CC ICK wild type protein. The present sequence represents an inhibitor of
XX      CC cyclin dependent kinase (ICK) protein of the invention
XX      SQ      Sequence 10 AA;
  Query Match      81.2%; Score 26; DB 5; Length 10;
  Best Local Similarity 50.0%; Pred. No. 7.7;
  Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 EXEFPFXXE 10
Db      1 EIEAFFAAE 10

RESULT 4
ABG65672
ID      ABG65672 standard; protein; 87 AA.
XX      AC
XX      AC ABG65672;
XX      DT 27-AUG-2002 (first entry)
XX      DE OsICK 3 protein.
XX      KW Plant; inhibitor of cyclin dependent kinase; ICK.
XX      OS Oryza sativa.
XX      PN WO200228893-A2.
XX      PD 11-APR-2002.

```


XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX PA (CROP-) CROPDESIGN NV.
XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX PI Hatzfeld Y;
XX DR WPI; 2002-471311/50.
XX DR N-PSDB; ABK93952.
XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX PT to screen substrates, drugs or compounds which modulate ICK activity and
XX PT treat disorders characterized by an insufficient or excessive production
XX PT of ICK inhibitors.
XX PS Claim 48; Fig 4; 141pp; English.
XX CC This invention relates to the DNA and protein sequences of novel isolated
XX CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX CC the invention may be used for treating disorders characterised by
XX CC insufficient or excessive production of an ICK inhibitor. The protein of
XX CC the invention may also be used to screen for naturally-occurring ICK
XX CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX CC treat disorders characterised by insufficient or excessive production of
XX CC ICK protein, forms which have decreased or aberrant activity compared to
XX CC ICK wild type protein. The present sequence represents an inhibitor of
XX CC cyclin dependent kinase (ICK) protein of the invention
XX SQ Sequence 87 AA;
XX Query Match 81.2%; Score 26; DB 5; Length 87;
XX Best Local Similarity 50.0%; Pred. No. 69;
XX Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 EXEFPFXXXE 10
XX DB 67 EIEAFFAAAE 76
XX RESULT 5
XX ID ABG65676 standard; protein; 108 AA.
XX AC ABG65676;
XX XX 27-AUG-2002 (first entry)
XX DE Broom corn ICK protein.
XX XX Plant; inhibitor of cyclin dependent kinase; ICK.
XX OS Sorghum bicolor.
XX XX WO200228893-A2.
XX PN 11-APR-2002.
XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX XX (CROP-) CROPDESIGN NV.
XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX PI Hatzfeld Y;
XX DR WPI; 2002-471311/50.
XX DR N-PSDB; ABK93956.
XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX PT to screen substrates, drugs or compounds which modulate ICK activity and
XX PT treat disorders characterized by an insufficient or excessive production
XX PT of ICK inhibitors.
XX PS Claim 48; Fig 3; 141pp; English.
XX CC This invention relates to the DNA and protein sequences of novel isolated
XX CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX CC the invention may be used for treating disorders characterised by
XX CC insufficient or excessive production of an ICK inhibitor. The protein of
XX CC the invention may also be used to screen for naturally-occurring ICK
XX CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX CC treat disorders characterised by insufficient or excessive production of
XX CC ICK protein, forms which have decreased or aberrant activity compared to
XX CC ICK wild type protein. The present sequence represents an inhibitor of
XX CC cyclin dependent kinase (ICK) protein of the invention
XX SQ Sequence 108 AA;
XX Query Match 81.2%; Score 26; DB 5; Length 108;
XX Best Local Similarity 50.0%; Pred. No. 86;
XX Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 EXEFPFXXXE 10
XX DB 67 EIEAFFAAAE 76
XX RESULT 6
XX ID ABG65670 standard; protein; 262 AA.
XX AC ABG65670;
XX XX 27-AUG-2002 (first entry)
XX DE OsiCK 2 protein.
XX XX Plant; inhibitor of cyclin dependent kinase; ICK.
XX OS Oryza sativa.
XX XX WO200228893-A2.
XX PN 11-APR-2002.
XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX XX (CROP-) CROPDESIGN NV.
XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX PI Hatzfeld Y;
XX DR WPI; 2002-471311/50.
XX DR N-PSDB; ABK93958.
XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX PT to screen substrates, drugs or compounds which modulate ICK activity and
XX PT treat disorders characterized by an insufficient or excessive production
XX PT of ICK inhibitors.
XX PS Claim 48; Fig 3; 141pp; English.
XX CC This invention relates to the DNA and protein sequences of novel isolated
XX CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX CC the invention may be used for treating disorders characterised by
XX CC insufficient or excessive production of an ICK inhibitor. The protein of
XX CC the invention may also be used to screen for naturally-occurring ICK
XX CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX CC treat disorders characterised by insufficient or excessive production of
XX CC ICK protein, forms which have decreased or aberrant activity compared to
XX CC ICK wild type protein. The present sequence represents an inhibitor of
XX CC cyclin dependent kinase (ICK) protein of the invention
XX SQ Sequence 108 AA;
XX Query Match 81.2%; Score 26; DB 5; Length 108;
XX Best Local Similarity 50.0%; Pred. No. 86;
XX Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 EXEFPFXXXE 10
XX DB 67 EIEAFFAAAE 76
XX RESULT 6
XX ID ABG65670 standard; protein; 262 AA.
XX AC ABG65670;
XX XX 27-AUG-2002 (first entry)
XX DE OsiCK 2 protein.
XX XX Plant; inhibitor of cyclin dependent kinase; ICK.
XX OS Oryza sativa.
XX XX WO200228893-A2.
XX PN 11-APR-2002.
XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX XX (CROP-) CROPDESIGN NV.
XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX PI Hatzfeld Y;
XX DR WPI; 2002-471311/50.
XX DR N-PSDB; ABK93958.
XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
XX PT to screen substrates, drugs or compounds which modulate ICK activity and
XX PT treat disorders characterized by an insufficient or excessive production
XX PT of ICK inhibitors.
XX PS Claim 48; Fig 3; 141pp; English.
XX CC This invention relates to the DNA and protein sequences of novel isolated
XX CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
XX CC the invention may be used for treating disorders characterised by
XX CC insufficient or excessive production of an ICK inhibitor. The protein of
XX CC the invention may also be used to screen for naturally-occurring ICK
XX CC substrates, drugs or compounds which modulate ICK activity, as well as to
XX CC treat disorders characterised by insufficient or excessive production of
XX CC ICK protein, forms which have decreased or aberrant activity compared to
XX CC ICK wild type protein. The present sequence represents an inhibitor of
XX CC cyclin dependent kinase (ICK) protein of the invention
XX SQ Sequence 108 AA;
XX Query Match 81.2%; Score 26; DB 5; Length 108;
XX Best Local Similarity 50.0%; Pred. No. 86;
XX Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX QY 1 EXEFPFXXXE 10
XX DB 67 EIEAFFAAAE 76
XX RESULT 6
XX ID ABG65670 standard; protein; 262 AA.
XX AC ABG65670;
XX XX 27-AUG-2002 (first entry)
XX DE OsiCK 2 protein.
XX XX Plant; inhibitor of cyclin dependent kinase; ICK.
XX OS Oryza sativa.
XX XX WO200228893-A2.
XX PN 11-APR-2002.
XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX XX (CROP-) CROPDESIGN NV.
XX PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
XX PI Hatzfeld Y;
XX DR WPI; 2002-471311/50.
XX DR N-PSDB; ABK93956.

CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 SQ Sequence 262 AA;

Query Match 81.2%; Score 26; DB 5; Length 262;
 Best Local Similarity 50.0%; Pred. No. 2.1e-02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
 |||||
 Db 217 ELEAFFAAE 226

RESULT 7
 ABG65733
 ID ABG65733 standard; peptide; 10 AA.
 XX
 AC ABG65733;

XX 27-AUG-2002 (first entry)
 XX Plant ICK protein conserved motif 1 #41.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.

XX Arabidopsis thaliana.

OS WO200228893-A2.

PN 11-APR-2002.

PD 29-JUN-2001; 2001WO-IB001492.

PF 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

XX (CROP-) CROPDESIGN NV.

PA Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

PI Hatzfeld Y;

XX WPI; 2002-471311/50.

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.

XX Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX

SQ Sequence 10 AA;

Query Match 78.1%; Score 25; DB 5; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
 |||||

Db 1 EIEDFFASAE 10

RESULT 8

ABG65739

ID ABG65739 standard; peptide; 10 AA.

XX AC ABG65739;

XX 27-AUG-2002 (first entry)

XX Plant ICK protein conserved motif 1 #47.

XX Plant; inhibitor of cyclin dependent kinase; ICK.

XX Oryza sativa.

PN WO200228893-A2.

PD 11-APR-2002.

PF 29-JUN-2001; 2001WO-IB001492.

XX 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

XX (CROP-) CROPDESIGN NV.

XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

PI Hatzfeld Y;

XX WPI; 2002-471311/50.

XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

PT to screen substrates, drugs or compounds which modulate ICK activity and

PT treat disorders characterized by an insufficient or excessive production

PT of ICK inhibitors.

XX Disclosure; Page 14; 141pp; English.

XX This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX

SQ Sequence 10 AA;

Query Match 78.1%; Score 25; DB 5; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
 |||||

Db 1 ELEAFFAAE 10

RESULT 9

AAB26246

ID AAB26246 standard; protein; 46 AA.

XX AC AAB26246;

XX 17-JAN-2001 (first entry)

XX Rice cyclin-dependent kinase inhibitor #1.

XX Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;

KW cell growth; herbicide.
 XX
 OS Oryza sativa.
 XX
 PN WC200060087-A2.
 XX
 XX
 PD 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US009106.
 PF
 XX 07-APR-1999; 99US-0128192P.
 XX
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX Klein TM, Weng Z, Cahoon RE;
 PI
 XX WPI; 2000-679375/66.
 DR
 DR N-PSDB; AAA95277.
 XX
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 XX Claim 10; Page 40; 58pp; English.
 XX
 XX The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX
 XX Sequence 46 AA;
 SQ

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXXE 10
 Db 6 ELEAFPAEE 15
 |||||
 |||||

RESULT 10
 AAP01941
 ID AAP01941 standard; protein; 46 AA.
 XX
 AC AAP01941;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Rice Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.
 XX
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
 KW plant growth inhibitor.
 XX
 OS Oryza sativa.
 XX
 PN WC200060087-A2.
 XX
 XX 12-OCT-2000.
 PD
 XX 06-APR-2000; 2000WO-US009106.
 PF
 XX 07-APR-1999; 99US-0128192P.
 XX
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX Klein TM, Weng Z, Cahoon RE;
 PI
 XX WPI; 2000-679375/66.
 DR
 DR N-PSDB; AAA95277.

DR N-PSDB; AAN02391.
 XX
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 XX Claim 10; Page 40; 58pp; English.
 XX
 XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the rice CDKI clone rsr9n.pk003.g12 as described
 CC in the method of the invention
 XX
 XX Sequence 46 AA;
 SQ

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXXE 10
 Db 6 ELEAFPAEE 15
 |||||
 |||||

RESULT 11
 AAP01953
 ID AAP01953 standard; protein; 60 AA.
 XX
 AC AAP01953;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0117.h4.
 XX
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 KW plant growth inhibitor.
 XX
 OS Glycine max.
 XX
 PN WC200060087-A2.
 XX
 XX 12-OCT-2000.
 PD
 XX 06-APR-2000; 2000WO-US009106.
 PF
 XX 07-APR-1999; 99US-0128192P.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX Klein TM, Weng Z, Cahoon RE;
 PI
 XX WPI; 2000-679375/66.
 DR
 DR N-PSDB; AAN02403.
 XX
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 XX Claim 10; Fig 1; 58pp; English.
 XX
 XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic

CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the soybean CDKI clone s12.pk0117.h4 as
 CC described in the method of the invention

XX Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10
 | | | | |
 Db 19 ELEDFFAAE 28

RESULT 12
 AAB27255
 ID AAB27255 standard; protein; 60 AA.

XX AAB27255;

DT 17-JAN-2001 (first entry)

DE Soybean cyclin-dependent kinase inhibitor #4.

KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
 KW CDKI; cell growth; herbicide.

OS Glycine max.

PN WO200060087-A2.

PD 12-OCT-2000.

PF 06-APR-2000; 2000WO-US009106.

PR 07-APR-1999; 99US-0128192P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;

DR WPI; 2000-679375/66.

DR N-PSDB; AAA95289.

PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

PS Claim 10; Fig 1; 58pp; English.

CC The present sequence is the soybean cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a soybean seedling
 CC cDNA library for sequences similar to those encoding the CDKI from
 CC Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI
 CC is involved in the cell cycle, and may promote or inhibit cell division
 CC and growth. The protein and its coding sequence are useful in the
 CC production of transgenic plants which produce increased or decreased
 CC amounts of the CDKI protein, in the identification of herbicides, in
 CC genetic and physical mapping and in the isolation of the CDKI gene in
 CC other organisms

XX Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10
 | | | | |

Db 19 ELEDFFAAE 28

RESULT 13

ABG5673

ID ABG5673 standard; protein; 90 AA.

XX AAG565673;

DT 27-AUG-2002 (first entry)

DE Rice Os ICK associated peptide.

KW Plant; inhibitor of cyclin dependent kinase; ICK.

OS Oryza sativa.

PN WO200228893-A2.

XX 11-APR-2002.

PF 29-JUN-2001; 2001WO-IB001492.

PR 14-JUL-2000; 2000US-0218471P.

PR 13-OCT-2000; 2000US-0241219P.

PA (CROP-) CROPDESIGN NV.

PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

PI Hatzfeld Y;

DR WPI; 2002-471311/50.

PT Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.

PS Claim 48; Disclosure; 141pp; English.

CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention

XX Sequence 90 AA;

Query Match 78.1%; Score 25; DB 5; Length 90;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10
 | | | | |

Db 50 ELEAFPAEE 59

RESULT 14

AAB27251

ID AAB27251 standard; protein; 99 AA.

XX AAB27251;

DT 17-JAN-2001 (first entry)

DE Rice cyclin-dependent kinase inhibitor #2.

KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;

KW cell growth; herbicide.
 XX Oryza sativa.
 OS WO200060087-A2.
 XX
 XX PD 12-OCT-2000.
 XX
 XX PF 06-APR-2000; 2000WO-US009106.
 XX
 XX PR 07-APR-1999; 99US-0128192P.
 XX
 XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX PI Klein TM, Weng Z, Cahoon RE;
 XX WPI; 2000-679375/66.
 DR N-PSDB; AAA95285.
 XX
 XX PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 XX PS Claim 10; Fig 1; 58pp; English.
 XX
 XX CC The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA
 CC library for sequences similar to those encoding the CDKI from Chenopodium
 CC rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX
 XX SQ Sequence 99 AA;
 Query Match 78.1%; Score 25; DB 3; Length 99;
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXXE 10
 DB 59 ELEAFFAAEE 68
 Search completed: October 26, 2004, 15:36:54
 Job time : 57.7692 secs

DR N-PSDB; AAN02399.
 XX
 XX PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 XX PS Claim 10; Fig 1; 58pp; English.
 XX
 XX CC The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the rice CDKI clone rsr9n.pk003.g12.fis as
 CC described in the method of the invention
 XX
 XX SQ Sequence 99 AA;
 Query Match 78.1%; Score 25; DB 3; Length 99;
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXXE 10
 DB 59 ELEAFFAAEE 68
 Search completed: October 26, 2004, 15:36:54
 Job time : 57.7692 secs

RESULT 15
 AAP01949
 ID AAP01949 standard; protein; 99 AA.
 XX
 XX AC AAP01949;
 XX
 XX DT 01-NOV-2001 (first entry)
 XX
 XX DE Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.fis.
 XX
 XX KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
 KW plant growth inhibitor.
 XX
 XX OS Oryza sativa.
 XX
 XX FN WO200060087-A2.
 XX
 XX PD 12-OCT-2000.
 XX
 XX PF 06-APR-2000; 2000WO-US009106.
 XX
 XX PR 07-APR-1999; 99US-0128192P.
 XX
 XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 XX PI Klein TM, Weng Z, Cahoon RE;
 XX WPI; 2000-679375/66.
 DR

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 16.5385 Seconds
(without alignments)
40.099 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFPFXXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	75.0	222	4	US-09-526-597D-4
2	24	75.0	583	3	US-09-311-311C-24
3	23	71.9	117	4	US-09-107-532A-6482
4	23	71.9	117	4	US-09-134-000C-5761
5	23	71.9	117	4	US-09-134-000C-6140
6	23	71.9	209	4	US-09-526-597D-2
7	23	71.9	860	4	US-09-248-796A-18585
8	23	71.9	966	4	US-09-688-188B-154
9	23	71.9	966	4	US-09-291-417D-154
10	23	71.9	968	4	US-09-688-188B-155
11	23	71.9	968	4	US-09-291-417D-107
12	23	71.9	968	4	US-09-291-417D-155
13	23	71.9	968	4	US-09-198-452A-1014
14	22	68.8	207	4	US-09-543-681A-7484
15	22	68.8	248	4	US-09-985-335-8
16	22	68.8	313	3	US-09-410-372-8
17	22	68.8	313	3	US-09-248-796A-25757
18	22	68.8	359	4	US-09-328-352-4855
19	22	68.8	408	4	US-09-985-335-3
20	22	68.8	440	3	US-09-410-372-3
21	22	68.8	440	3	US-08-860-519-12
22	22	68.8	600	3	US-09-489-039A-7380
23	22	68.8	600	3	US-09-297-937C-9
24	22	68.8	615	3	US-09-440-325A-1
25	22	68.8	694	3	US-09-846-996A-1
26	22	68.8	694	4	US-09-105-058C-23
27	22	68.8	722	4	US-09-105-058C-23

28 22 68.8 757 4 US-09-177-650-89 Sequence 89, Appli
29 22 68.8 844 4 US-09-813-148-4 Sequence 4, Appli
30 22 68.8 844 4 US-09-590-304-4 Sequence 4, Appli
31 22 68.8 844 4 US-09-492-361-34 Sequence 34, Appli
32 22 68.8 871 4 US-09-105-058C-20 Sequence 20, Appli
33 22 68.8 872 4 US-09-177-650-2 Sequence 2, Appli
34 22 68.8 930 4 US-09-177-650-96 Sequence 96, Appli
35 22 68.8 1276 3 US-09-297-937C-13 Sequence 13, Appli
36 21 65.6 29 4 US-09-079-030-74 Sequence 74, Appli
37 21 65.6 40 4 US-09-270-767-34838 Sequence 34838, A
38 21 65.6 40 4 US-09-270-767-50055 Sequence 50055, A
39 21 65.6 60 4 US-09-583-110-4465 Sequence 4465, Ap
40 21 65.6 73 4 US-09-621-976-5436 Sequence 5436, Ap
41 21 65.6 78 4 US-09-134-000C-4647 Sequence 4647, Ap
42 21 65.6 94 3 US-09-134-001C-4940 Sequence 4940, Ap
43 21 65.6 102 4 US-09-107-532A-5863 Sequence 5863, Ap
44 21 65.6 104 4 US-09-107-532A-4385 Sequence 4385, Ap
45 21 65.6 106 4 US-09-270-767-61925 Sequence 61925, A

ALIGNMENTS

RESULT 1
US-09-526-597D-4
; Sequence 4, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-4

Query Match 75.0%; Score 24; DB 4; Length 222;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXXE 10
DB 181 EMEFFAYAE 190

RESULT 2
US-09-311-311C-24
; Sequence 24, Application US/093111111C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CHAIN

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; LOCATION: (1)....(583)
; OTHER INFORMATION: GRASP65 protein
US-09-311-311C-24

Query Match      75.0%; Score 24; DB 3; Length 583;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 144 ESEDFTLIE 153

RESULT 3
US-09-107-532A-6482
; Sequence 6482, Application US/09107532A
; Patent No. 6563275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...117
; SEQUENCE DESCRIPTION: SEQ ID NO: 6482:
US-09-107-532A-6482

Query Match      71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

; LOCATION: (1)....(583)
; OTHER INFORMATION: GRASP65 protein
US-09-311-311C-24

Query Match      75.0%; Score 24; DB 3; Length 583;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 144 ESEDFTLIE 153

RESULT 3
US-09-107-532A-6482
; Sequence 6482, Application US/09107532A
; Patent No. 6563275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...117
; SEQUENCE DESCRIPTION: SEQ ID NO: 6482:
US-09-107-532A-6482

Query Match      71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

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RESULT 4
US-09-134-000C-5761
; Sequence 5761, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5761
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5761

Query Match      71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

RESULT 5
US-09-134-000C-6140
; Sequence 6140, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6140
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6140

Query Match      71.9%; Score 23; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
Db 65 EEESFFMWE 74

RESULT 6
US-09-526-597D-2
; Sequence 2, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-2

Query Match 71.9%; Score 23; DB 4; Length 209;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
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Db 164 ELEDFFQVAE 173

RESULT 7
US-09-248-796A-18585
; Sequence 18585, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18585
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18585

Query Match 71.9%; Score 23; DB 4; Length 860;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
| | | | |
Db 298 ELETFEKKRE 307

RESULT 8
US-09-688-188B-154
; Sequence 154, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-688-188B-154

Query Match 71.9%; Score 23; DB 4; Length 966;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EXEXFFXXXE 10
| | | | |
Db 933 EQEMFFKLSE 942

RESULT 9
US-09-291-417D-154
; Sequence 154, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-154

Query Match 71.9%; Score 23; DB 4; Length 966;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
| | | | |
Db 933 EQEMFFKLSE 942

RESULT 10
US-09-688-188B-107
; Sequence 107, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-107

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
| | | | |
Db 934 EQEMFFKLSE 943

RESULT 11
US-09-688-188B-155

; Sequence 155, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 155
; TYPE: PRT
; LENGTH: 968
; ORGANISM: Homo sapiens
US-09-688-188B-155

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
| | | | |
Db 934 EQEMFFKLS 943

RESULT 12
US-09-291-417D-107
; Sequence 107, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 107
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-107

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
| | | | |
Db 934 EQEMFFKLS 943

RESULT 13
US-09-291-417D-155
; Sequence 155, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D

; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 155
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-155

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
| | | | |
Db 934 EQEMFFKLS 943

RESULT 14
US-09-198-452A-1014
; Sequence 1014, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5849
; SEQ ID NO 1014
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1014

Query Match 68.8%; Score 22; DB 4; Length 207;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EXEXFF 6
| | | | |
Db 123 EAETFF 128

RESULT 15
US-09-543-681A-7484
; Sequence 7484, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY, BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7484
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7484

Query Match 68.8%; Score 22; DB 4; Length 248;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EXEXFF 6

Db 128 ESEAFF 133

Search completed: October 26, 2004, 15:34:20
Job time : 17.5385 secs

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 143.846 Seconds
(without alignments)
22.507 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 32

Sequence: 1 EXEFFFFXXE 10

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	81.2	87	US-10-333-006-12	Sequence 12, Appl
2	26	81.2	108	US-10-333-006-16	Sequence 16, Appl
3	26	81.2	225	US-10-437-963-198574	Sequence 198574,
4	26	81.2	262	US-10-333-006-10	Sequence 10, Appl
5	26	81.2	417	US-10-437-963-195115	Sequence 195115,
6	25	78.1	90	US-10-333-006-13	Sequence 13, Appl
7	25	78.1	95	US-10-767-701-36263	Sequence 36263, A
8	25	78.1	194	US-10-333-006-44	Sequence 44, Appl
9	25	78.1	194	US-10-437-963-120870	Sequence 120870,
10	25	78.1	205	US-10-424-599-182928	Sequence 182928,
11	25	78.1	218	US-10-437-963-128205	Sequence 128205,
12	25	78.1	248	US-10-425-114-59718	Sequence 59718, A
13	25	78.1	255	US-10-425-114-61054	Sequence 61054, A

14	78.1	401	14	US-10-369-493-22727	Sequence 22727, A
15	78.1	401	14	US-10-369-493-22728	Sequence 22728, A
16	78.1	401	14	US-10-369-493-22808	Sequence 22808, A
17	75.0	53	15	US-10-333-006-17	Sequence 17, Appl
18	75.0	69	16	US-10-767-701-53471	Sequence 53471, A
19	75.0	137	9	US-09-733-507-14	Sequence 14, Appl
20	75.0	137	15	US-10-451-139-13	Sequence 13, Appl
21	75.0	176	15	US-10-424-599-212181	Sequence 212181,
22	75.0	196	9	US-09-733-507-15	Sequence 15, Appl
23	75.0	196	15	US-10-451-139-15	Sequence 15, Appl
24	75.0	205	15	US-10-424-599-235800	Sequence 235800,
25	75.0	222	15	US-10-688-291-4	Sequence 4, Appl
26	75.0	222	15	US-10-451-139-21	Sequence 21, Appl
27	75.0	246	14	US-10-104-047-2319	Sequence 2319, Ap
28	75.0	340	14	US-10-013-477-14	Sequence 14, Appl
29	75.0	570	16	US-10-437-963-177783	Sequence 177783,
30	75.0	617	16	US-10-437-963-177786	Sequence 177786,
31	75.0	660	15	US-10-282-122A-55169	Sequence 55169, A
32	75.0	786	14	US-10-369-493-6228	Sequence 6228, Ap
33	75.0	795	14	US-10-156-761-9635	Sequence 9635, Ap
34	75.0	905	13	US-10-114-893-127	Sequence 127, Appl
35	75.0	915	9	US-09-880-192-59	Sequence 59, Appl
36	75.0	915	14	US-10-427-348-59	Sequence 59, Appl
37	71.9	72	11	US-09-864-408A-8656	Sequence 8656, Ap
38	71.9	176	9	US-09-733-507-11	Sequence 11, Appl
39	71.9	176	15	US-10-451-139-10	Sequence 10, Appl
40	71.9	191	9	US-09-733-507-2	Sequence 2, Appl
41	71.9	191	9	US-09-733-507-10	Sequence 10, Appl
42	71.9	191	15	US-10-451-139-2	Sequence 2, Appl
43	71.9	209	15	US-10-688-291-2	Sequence 2, Appl
44	71.9	209	15	US-10-451-139-19	Sequence 19, Appl
45	71.9	276	14	US-10-156-761-9715	Sequence 9715, Ap

ALIGNMENTS

RESULT 1
US-10-333-006-12
Sequence 12, Application US/10333006
Publication No. US20040019926A1
GENERAL INFORMATION:
APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
APPLICANT: Peres Bota, Adrian Marius
APPLICANT: Drouot, Anne-Marie
APPLICANT: Mironov, Vladimir
APPLICANT: Inz, Dirk
APPLICANT: Hatzfeld, Yves
TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
FILE REFERENCE: 1187-13
CURRENT APPLICATION NUMBER: US/10/333,006
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: PCT/IB01/01492
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/218,471
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/241,219
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 87
TYPE: PRT
ORGANISM: Oryza sativa
US-10-333-006-12

Query Match 81.2%; Score 26; DB 15; Length 87;
Best Local Similarity 50.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFFFFXXE 10

DB 67 EIEAFFAAAE 76

RESULT 2
US-10-333-006-16
; Sequence 16, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Sorghum bicolor
US-10-333-006-16

Query Match 81.2%; Score 26; DB 15; Length 108;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10
DB 67 EIEAFFAAAE 76

RESULT 3
US-10-437-963-198574
; Sequence 198574, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198574
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9421C.1.pep
US-10-437-963-198574

Query Match 81.2%; Score 26; DB 16; Length 225;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10

Db 173 EIEAFFAAAE 182
RESULT 4
US-10-333-006-10
; Sequence 10, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1lle S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-10

Query Match 81.2%; Score 26; DB 15; Length 262;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10
DB 217 EIEAFFAAAE 226

RESULT 5
US-10-437-963-195115
; Sequence 195115, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195115
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91095C.1.pep
US-10-437-963-195115

Query Match 81.2%; Score 26; DB 16; Length 417;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEFPFXXE 10

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Db 372 EIEAFFAAAE 381
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RESULT 6
US-10-333-006-13
; Sequence 13, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-13
Query Match 78.1%; Score 25; DB 15; Length 90;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
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Db 50 ELEAFFAAAE 59
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RESULT 7
US-10-767-701-36263
; Sequence 36263, Application US/10767701
; Publication No. US20040172664A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 36263
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C86129_1.pep
US-10-767-701-36263
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Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
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Db 54 EMEFFFAAE 63
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RESULT 8
US-10-333-006-44
; Sequence 44, Application US/10333006
; Publication No. US20040019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A111e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz., Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 1187-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-44
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Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
| | | |
Db 154 ELEAFFAAAE 163
| | | |
RESULT 9
US-10-437-963-120870
; Sequence 120870, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120870
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23950C.1.pep
US-10-437-963-120870
Query Match 78.1%; Score 25; DB 16; Length 194;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 154 ELEAFFAAAE 163
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RESULT 10
US-10-424-599-182928
; Sequence 182928, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182928
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928
Query Match 78.1%; Score 25; DB 15; Length 205;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 EXEXFFXXE 10
Db 164 EEEFFFAAE 173

RESULT 11
US-10-437-963-128205
; Sequence 128205, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128205
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(218)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30581C.1.pep
US-10-437-963-128205
Query Match 78.1%; Score 25; DB 16; Length 218;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 EXEXFFXXE 10
Db 180 EEEFFFAAE 189

RESULT 12
US-10-425-114-59718
; Sequence 59718, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59718
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-047-G6_FLI.pep
US-10-425-114-59718
Query Match 78.1%; Score 25; DB 15; Length 248;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 EXEXFFXXE 10
Db 207 EMEFFFAAE 216

RESULT 13
US-10-425-114-61054
; Sequence 61054, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61054
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3729-047-A7_FLI.pep
US-10-425-114-61054
Query Match 78.1%; Score 25; DB 15; Length 255;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 EXEXFFXXE 10
Db 214 EMEFFFAAE 223

RESULT 14
US-10-369-493-22727
; Sequence 22727, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22727
LENGTH: 401
TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(401)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22727

Query Match 78.1%; Score 25; DB 14; Length 401;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 351 ETESFFQAKE 360

RESULT 15
US-10-369-493-22728
Sequence 22728, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22728
LENGTH: 401
TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(401)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22728

Query Match 78.1%; Score 25; DB 14; Length 401;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
Db 351 ETESFFQAKE 360

Search completed: October 26, 2004, 15:33:30
Job time : 144.846 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 26, 2004, 15:27:13 ; Search time 13.8462 Seconds
(without alignments)
69.490 Million cell updates/sec

Title: US-09-574-735c-36
Perfect score: 32
Sequence: 1 EXEXFFXXE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	78.1	62	2 B71318	conserved hypothetical
2	25	78.1	380	2 S62523	septin homolog - f
3	25	78.1	799	2 T02656	probable salt-indu
4	24	75.0	196	2 T09968	cyclin-dependent k
5	24	75.0	299	2 T15928	hypothetical prote
6	24	75.0	315	2 C83945	stage V sporulatio
7	24	75.0	660	2 A81704	DNA ligase TC0423
8	24	75.0	663	2 C71551	probable DNA ligas
9	24	75.0	786	2 T26811	hypothetical prote
10	24	75.0	808	2 T04092	phospholipase D (E
11	23	71.9	79	2 B81014	hypothetical prote
12	23	71.9	137	2 B86188	YUP8H12.5 (impor
13	23	71.9	140	2 C97710	nucleoside-diphosp
14	23	71.9	146	2 T71263	probable flavodoxi
15	23	71.9	146	2 A69950	conserved hypothet
16	23	71.9	155	2 T42687	hypothetical prote
17	23	71.9	191	2 T01132	cyclin-dependent k
18	23	71.9	200	2 AE1632	hypothetical prote
19	23	71.9	209	2 T46140	hypothetical prote
20	23	71.9	335	2 S76519	hypothetical prote
21	23	71.9	364	2 T20748	hypothetical prote
22	23	71.9	474	2 T31064	hypothetical prote
23	23	71.9	829	2 F75415	phosphoenolpyruvat
24	23	71.9	1251	2 A56677	neuronal cell cycl
25	23	71.9	1425	2 T22493	hypothetical prote
26	23	71.9	1673	2 T50806	complement compone
27	22	68.8	142	2 C82283	nucleoside diphosp
28	22	68.8	165	2 AB0851	hypothetical prote
29	22	68.8	165	2 S70217	sipE protein - Sal

30	22	68.8	165	2 A57357	sick protein - Sal
31	22	68.8	195	2 H96532	hypothetical prote
32	22	68.8	218	2 H69060	chromosome partiti
33	22	68.8	230	2 C75552	hypothetical prote
34	22	68.8	233	2 T33829	hypothetical prote
35	22	68.8	243	2 AB0832	conserved hypothet
36	22	68.8	257	2 AB1208	extragenic suppres
37	22	68.8	257	2 AE1564	extragenic suppres
38	22	68.8	261	2 E69455	conserved hypothet
39	22	68.8	269	1 A27067	calretinin - chick
40	22	68.8	271	1 A60253	calretinin - human
41	22	68.8	271	1 S25006	calretinin - rat
42	22	68.8	313	2 G02020	p37NB - human
43	22	68.8	363	2 E83970	UDP-N-acetylglucos
44	22	68.8	382	2 AE2754	two component sens
45	22	68.8	382	2 C97535	nitrogen regulatio

ALIGNMENTS

RESULT 1

B71318
conserved hypothetical protein TP0490 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: B71318
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mcd
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: B71318
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <COL>
A:Cross-references: UNIPROT:O83503; GB:AE001225; GB:AE000520; NID:G3322775; PIDN:AA6654
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0490

Query Match 78.1%; Score 25; DB 2; Length 62;
Best Local Similarity 50.0%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
DB 52 EAEDFFGSAE 61

RESULT 2

S62523
septin homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: T41191; T41431; T39129; S62523
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, April 1999
A:Reference number: Z21976
A:Accession: T41191
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-380 <LYN>
A:Cross-references: UNIPROT:Q09883; EMBL:AL049662; PIDN:CAB41232.1; GSPDB:GN00068; SPDB
A:Experimental source: strain 972h; cosmid c188
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21993
A:Accession: T41431
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-380 <SEB>

A;Cross-references: EMBL:AL032824; PIDN:CA37422.1; GSPDB:GN00068; SPDB:SPCC584.09
 A;Experimental source: strain 972h-; cosmid c584
 R;Lye, G.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z21830
 A;Accession: T39129
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-380 <LY2>
 A;Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91517.1; PID:g1052538; SPDB:SPACB
 C;Genetics: <JFINI>
 A;Gene: SPCC188.12
 A;Map position: 3
 A;Introns: 20/2
 C;Genetics: <SEE2>
 A;Gene: SPCC584.09
 A;Map position: 3
 A;Introns: 20/2
 C;Genetics: <LY23>
 A;Gene: SPDB:SPAC8A4.07
 A;Map position: 1
 A;Introns: 20/2
 C;Superfamily: Saccharomyces cerevisiae cell division control protein CDC10
 Query Match 78.1%; Score 25; DB 2; Length 380;
 Best Local Similarity 50.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 DB 330 ETESFQAKE 339
 RESULT 3
 T02656
 N;Alternate names: hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02656; H84664
 R;Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy
 submitted to the EMBL Data Library, August 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
 A;Reference number: Z14685
 A;Accession: T02656
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-799 <ROU>
 A;Cross-references: UNIPROT:O81028; EMBL:AC005168; NID:g3426033; PID:g3426046
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: H84664
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-799 <STO>
 A;Cross-references: GB:AE002093; NID:g3426046; PIDN:AAC32245.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: F12C20.17; At2g26790
 A;Map position: 2
 Query Match 78.1%; Score 25; DB 2; Length 799;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 DB 511 EAEDFFSLE 520

RESULT 4

T09968
 cyclin-dependent kinase inhibitor protein - red goosefoot
 C;Species: Chenopodium rubrum (red goosefoot)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T09968
 R;Fountain, M.D.; Renz, A.; Beck, E.
 submitted to the EMBL Data Library, November 1997
 A;Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic
 A;Reference number: Z16910
 A;Accession: T09968
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-196 <FOU>
 A;Cross-references: UNIPROT:O48597; EMBL:AJ002173
 A;Experimental source: photoautotrophic cells derived from hypocotyl tissue
 C;Genetics:
 A;Gene: CDK11
 C;Keywords: protein kinase inhibitor

Query Match 75.0%; Score 24; DB 2; Length 196;
 Best Local Similarity 50.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
 DB 155 EIEFFFAVAE 164

RESULT 5

T15928
 hypothetical protein EED8.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T15928
 R;Chissee, S.
 submitted to the EMBL Data Library, July 1995
 A;Description: The sequence of C. elegans cosmid EED8.
 A;Reference number: Z18428
 A;Accession: T15928
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-239 <CHI>
 A;Cross-references: UNIPROT:Q09529; EMBL:U23484; NID:g733597; PID:g733599; PIDN:AAC46762
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESP.EED8.2
 A;Introns: 84/3; 133/3; 275/3

Query Match 75.0%; Score 24; DB 2; Length 299;
 Best Local Similarity 50.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
 DB 134 EESFFSLHE 143

RESULT 6

C83945
 stage V sporulation protein X BH2363 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: C83945
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: C83945
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-315 <STO>

```

A;Cross-references: UNIPROT:Q9KAC6; GB:BA000004; NID:g10174886; PIDN:BA0060
A;Experimental source: strain C-125
C;Genetics:
C;Gene: BH2363
C;Superfamily: cfxQ protein

Query Match 75.0%; Score 24; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
Db 26 EEEFFHSEE 35

RESULT 7
A81704
DNA ligase TC0423 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 12-Jul-2004
C;Accession: A81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81704
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <TST>
A;Cross-references: UNIPROT:Q9PKP2; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3927
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
C;Gene: TC0423
C;Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 75.0%; Score 24; DB 2; Length 660;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
Db 91 ELEEFFSRTE 100

RESULT 8
C71551
Probable DNA ligase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 12-Jul-2004
C;Accession: C71551
R;Stephens, R.S.; Kallman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-663 <ARN>
A;Cross-references: UNIPROT:Q84148; GB:AE001288; GB:AE001273; NID:g3328545; PIDN:AA06773
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: dnlg
C;Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 75.0%; Score 24; DB 2; Length 663;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10
Db 91 ELEEFFSRTE 100

```

RESULT 9

T26811
 hypothetical protein Y41E3.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T26811
 R;McMurray, A.
 submitted to the EMBL Data Library, May 1997
 A;Reference number: Z20270
 A;Accession: T26811
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-786 <WIL>
 A;Cross-references: UNIPROT:O62431; EMBL:Z95559; PIDN:CAB08998.1; GSPDB:GN00022; CBSP:Y
 A;Experimental source: clone Y41E3
 C;Genetics:

A;Gene: CBSP:Y41E3.4
 A;Map position: 4
 A;Introns: 83/3; 195/3; 357/3; 573/2; 749/2
 C;Superfamily: human glutamine-tRNA ligase; glutamine-tRNA ligase homology

Query Match 75.0%; Score 24; DB 2; Length 786;
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10

Db 316 EEEKFFSAIE 325

RESULT 10

T04092
 phospholipase D (EC 3.1.4.4) - common tobacco
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T04092
 R;Lein, W.; Saalbach, G.
 submitted to the EMBL Data Library, May 1997
 A;Description: Characterization of tobacco phospholipase D.
 A;Reference number: Z15203
 A;Accession: T04092

A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-808 <LEI>

A;Cross-references: UNIPROT:P93400; EMBL:Z84822; NID:e1057206; PIDN:CAB06620.1; PID:e33
 A;Experimental source: strain SRI; tissue-type leaf
 C;Superfamily: phospholipase D, plant type
 C;Keywords: phosphoric diester hydrolase

Query Match 75.0%; Score 24; DB 2; Length 808;
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXXE 10

Db 293 ETEQFFQGTI 302

RESULT 11

B81014
 hypothetical protein NMB2037 [imported] - Neisseria meningitidis (strain MC58 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: B81014; F81956

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
 Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81014

A:Accession: A69950
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-146 <KUN>
A:Cross-references: UNIPROT:P45945; GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14521
A:Experimental source: strain 168
C:Genetics:
A:Gene: Yqck

Query Match 71.9%; Score 23; DB 2; Length 146;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFXXE 10
Db 81 EXEGFFAREE 90

Search completed: October 26, 2004, 15:40:10
Job time : 15.8462 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 55.7692 Seconds
(without alignments)
103.171 Million cell updates/sec

Title: US-09-574-735c-36
Perfect score: 32
Sequence: 1 EXEFPFXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	81.2	262	Q626G5	Q626G5 oryza sativ
2	26	81.2	262	BAD17213	BAD17213 oryza sat
3	25	78.1	62	O83503	O83503 treponema p
4	25	78.1	166	Q6T220	Q6T220 glycine max
5	25	78.1	166	AAS13377	AAS13377 glycine m
6	25	78.1	189	Q9LRY0	Q9LRY0 arabidopsis
7	25	78.1	192	Q9FS28	Q9FS28 pisum sativ
8	25	78.1	205	Q6T223	Q6T223 glycine max
9	25	78.1	205	AAS13374	AAS13374 glycine m
10	25	78.1	223	Q6L1B0	Q6L1B0 photobacter
11	25	78.1	223	CAG22039	CAG22039 photobact
12	25	78.1	242	Q7XDH8	Q7XDH8 oryza sativ
13	25	78.1	242	Q9FW65	Q9FW65 oryza sativ
14	25	78.1	293	Q92RW5	Q92RW5 rhizobium m
15	25	78.1	380	1 SPN6 SCHPO	O99883 schizosacch
16	25	78.1	436	Q8DZV3	Q8DZV3 streptococc
17	25	78.1	436	Q8B5K1	Q8B5K1 streptococc
18	25	78.1	618	Q7S542	Q7S542 neurospora
19	25	78.1	799	Q81028	Q81028 arabidopsis
20	24	75.0	123	Q6ZWH0	Q6ZWH0 homo sapien
21	24	75.0	123	BAC85533	BAC85533 homo sapi
22	24	75.0	148	Q67567	Q67567 digitaria s
23	24	75.0	185	Q8GT28	Q8GT28 lycopersico
24	24	75.0	196	Q7RH53	Q7RH53 plasmodium
25	24	75.0	196	Q48597	Q48597 chenopodium
26	24	75.0	198	Q5T222	Q5T222 glycine max
27	24	75.0	198	AAS13375	AAS13375 glycine m
28	24	75.0	210	Q8GT29	Q8GT29 lycopersico
29	24	75.0	222	Q9FKB5	Q9FKB5 arabidopsis
30	24	75.0	260	Q6C9I5	Q6C9I5 varrowia li
31	24	75.0	264	Q72U04	Q72U04 leptospira

32	24	75.0	264	2	Q8F150	Q8F150 leptospira
33	24	75.0	264	2	AAS69474	AAS69474 leptospir
34	24	75.0	299	1	YQO2 CAEEL	YQO2 CAEEL
35	24	75.0	315	2	Q9KAC6	Q9KAC6 bacillus ha
36	24	75.0	353	2	Q8S8B2	Q8S8B2 encephalito
37	24	75.0	370	2	Q7Q2A8	Q7Q2A8 anopheles g
38	24	75.0	439	1	GR65 HUMAN	GR65 HUMAN
39	24	75.0	445	1	GR65 MOUSE	GR65 MOUSE
40	24	75.0	445	2	Q7XV12	Q7XV12 mus musculu
41	24	75.0	450	1	GR65 RAT	GR65 RAT
42	24	75.0	537	2	Q7Z4P8	Q7Z4P8 rattus norv
43	24	75.0	633	2	Q8NDL2	Q8NDL2 homo sapien
44	24	75.0	660	1	DNLJ CHLMU	DNLJ CHLMU
45	24	75.0	663	1	DNLJ CHLTR	DNLJ CHLTR

ALIGNMENTS

RESULT 1

Q626G5 PRELIMINARY; PRT; 262 AA.
AC Q626G5; 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein P0486G03.18.
GN Name=P0486G03.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005002; BAD17213.1; -
DR InterPro: IPR003175; CDI.
DR Pfam: PF02234; CDI; 1.
SQ Hypothetical protein.
KW SEQUENCE 262 AA; 27138 MW; 42EC85C8276C0726 CRC64;

Query Match 81.2%; Score 26; DB 2; Length 262;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEFPFXXE 10

Db 217 EIEAFAAAE 226

RESULT 2

BAD17213 PRELIMINARY; PRT; 262 AA.
AC BAD17213; 10-MAY-2004 (T-EMBLrel. 27, Created)
DT 10-MAY-2004 (T-EMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein P0486G03.18.
GN P0486G03.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0486G03.18";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

```

DR EMBL: AP005002; BAD17213.1; -.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 27138 MW; 425C85C8276C0726 CRC64;

Query Match      81.2%; Score 26; DB 2; Length 262;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
| | | | |
Db 217 EIEAFFFAAE 226

RESULT 3
OB3503 ID O83503 PRELIMINARY; PRT; 62 AA.
AC O83503;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Hypothetical protein TP0490.
GN OrderedLocusNames=TP0490;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
DR EMBL: AE001225; AAC65477.1; -.
DR PIR: B71318; B71318.
DR TIGR: TP0490; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7230 MW; 6BD1E040146CFAD8 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 62;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
| | | | |
Db 52 EAEDFFGSAAE 61

RESULT 4
Q8T220 ID Q6T220 PRELIMINARY; PRT; 166 AA.
AC Q6T220;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein TP0490.
DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY439104; AAS13377.1; -.
DR GO: GO:0016301; F:kinase activity; IEA.

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DR InterPro: IPR003175; CDI.
DR Pfam: PF02334; CDI; 1.
KW Cyclin; Kinase.
FT NON_TER 166
SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
| | | | |
Db 127 ELEDFFAAAE 136

RESULT 5
AAS13377 ID AAS13377 PRELIMINARY; PRT; 166 AA.
AC AAS13377;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein TP0490.
DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Li S., Reverdatto S., Nielsen N.C.;
RT "cDNA of cell-cycle genes in soybean cotyledons."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY439104; AAS13377.1; -.
KW Cyclin; Kinase.
FT NON_TER 166
SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match      78.1%; Score 25; DB 2; Length 166;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXXE 10
| | | | |
Db 127 ELEDFFAAAE 136

RESULT 6
Q9LRY0 ID Q9LRY0 PRELIMINARY; PRT; 189 AA.
AC Q9LRY0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Similarity to cyclin-dependent kinase inhibitor protein (Cyclin-
DE dependent kinase inhibitor 5).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342510; PubMed=11449057;
 RA De Veylder L., Beeckman T., Beemster G.T.S., Krols L., Terras F.,
 RA Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.,
 RT "Functional analysis of Cyclin-dependent kinase inhibitors of
 RT Arabidopsis.",
 RL Plant Cell 13:1653-1668(2001).
 DR EMBL; AB028609; BAB02891.1; -;
 DR EMBL; AJ301556; CAC41619.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 189 AA; 21424 MW; A66041310E8DDE6 CRC64;
 Query Match 78.1%; Score 25; DB 2; Length 189;
 Best Local Similarity 50.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 Db 148 EIEEFFASAE 157
 RESULT 7
 ID Q9FS28 PRELIMINARY; PRT; 192 AA.
 AC Q9FS28;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cyclin dependent kinase inhibitor.
 GN Name=cki;
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Axillary bud;
 RA Shimizu-Sato S., Mori H.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029483; BAB20860.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 192 AA; 21921 MW; E76D734000885EB2 CRC64;
 Query Match 78.1%; Score 25; DB 2; Length 192;
 Best Local Similarity 50.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 Db 151 EIEEFFASAE 160
 RESULT 8
 ID Q6T223 PRELIMINARY; PRT; 205 AA.
 AC Q6T223;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1;1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li S., Reverdatto S., Nielsen N.C.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY439101; AAS13374.1; -;
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;
 Query Match 78.1%; Score 25; DB 2; Length 205;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 Db 164 EIEEFFASAE 173
 RESULT 9
 ID AAS13374 PRELIMINARY; PRT; 205 AA.
 AC AAS13374;
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 1;1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li S., Reverdatto S., Nielsen N.C.;
 RL "CDNA of cell-cycle genes in soybean cotyledons";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY439101; AAS13374.1; -;
 KW Cyclin; Kinase.
 SQ SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;
 Query Match 78.1%; Score 25; DB 2; Length 205;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EXEXFFXXE 10
 Db 164 EIEEFFASAE 173
 RESULT 10
 ID Q6LLB0 PRELIMINARY; PRT; 223 AA.
 AC Q6LLB0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein YCAQ.
 GN Name=YCAQ; OrderedLocNames=PPR0166;
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Photobacterium.
 OX NCBI_TaxID=74103;
 RN [1]
 RP SEQUENCE FROM N.A.

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RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378675; CAG22039.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
D 189 EKETFFTALE 198
Db

RESULT 11
CAG22039 PRELIMINARY; PRT; 223 AA.
ID CAG22039;
AC CAG22039;
DT 10-MAY-2004 (TRENBLrel. 27, Created)
DT 10-MAY-2004 (TRENBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein YCAQ.
GN YCAQ OR PBRB0166.
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ss9;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome Analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ss9;
RA Cestaro A.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR378675; CAG22039.1; -
KW Hypothetical protein.
SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
D 189 EKETFFTALE 198
Db

RESULT 12
Q7XDH8 PRELIMINARY; PRT; 242 AA.
ID Q7XDH8;
AC Q7XDH8;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative cyclin-dependent kinase inhibitor.
GN ORNames=OSUNB0094K03.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378675; CAG22039.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 223 AA; 25756 MW; F1DC29298B9C9C57 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
D 189 EKETFFTALE 198
Db

RESULT 13
Q9FW65 PRELIMINARY; PRT; 242 AA.
ID Q9FW65;
AC Q9FW65;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative cyclin-dependent kinase inhibitor.
GN Names=OSUNB0094K03.16;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC069145; AAG16867.1; -
DR Gramene; Q9FW65; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 242 AA; 26750 MW; F215A01234735928 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 242;
Best Local Similarity 50.0%; Pred. No. 2.4e-02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
D 202 ELEAFPAEE 211
Db

RESULT 13
Q9FW65 PRELIMINARY; PRT; 242 AA.
ID Q9FW65;
AC Q9FW65;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative cyclin-dependent kinase inhibitor.
GN Names=OSUNB0094K03.16;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC069145; AAG16867.1; -
DR Gramene; Q9FW65; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 242 AA; 26750 MW; F215A01234735928 CRC64;

Query Match 78.1%; Score 25; DB 2; Length 242;
Best Local Similarity 50.0%; Pred. No. 2.4e-02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFFXXE 10
D 202 ELEAFPAEE 211
Db

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OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Woldjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehmach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=1021;
RX MEDLINE=21369507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Lelaure V., Masuy D.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591784; CAC45297.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Complete proteome.
SQ SEQUENCE 293 AA; 32763 MW; BF6530C41BF9245A CRC64;

Query Match 78.1%; Score 25; DB 2; Length 293;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
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DB 60 EGEVFFAAE 69

RESULT 15
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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Septin homolog spn6.
GN Name=spn6; ORFNames=SFCC188.12, SFCC594.09;

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Search completed: October 26, 2004, 15:39:29

Wed Oct 27 09:35:41 2004

us-09-574-735c-36.rup

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Job time : 57.7692 secs